



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:54 AM UTC

PDB ID : 4D67 / pdb_00004d67
EMDB ID : EMD-2813
Title : Cryo-EM structures of ribosomal 80S complexes with termination factors and cricket paralysis virus IRES reveal the IRES in the translocated state
Authors : Muhs, M.; Hilal, T.; Mielke, T.; Skabkin, M.A.; Sanbonmatsu, K.Y.; Pestova, T.V.; Spahn, C.M.T.
Deposited on : 2014-11-10
Resolution : 9.00 Å (reported)
Based on initial model : 4CXD

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

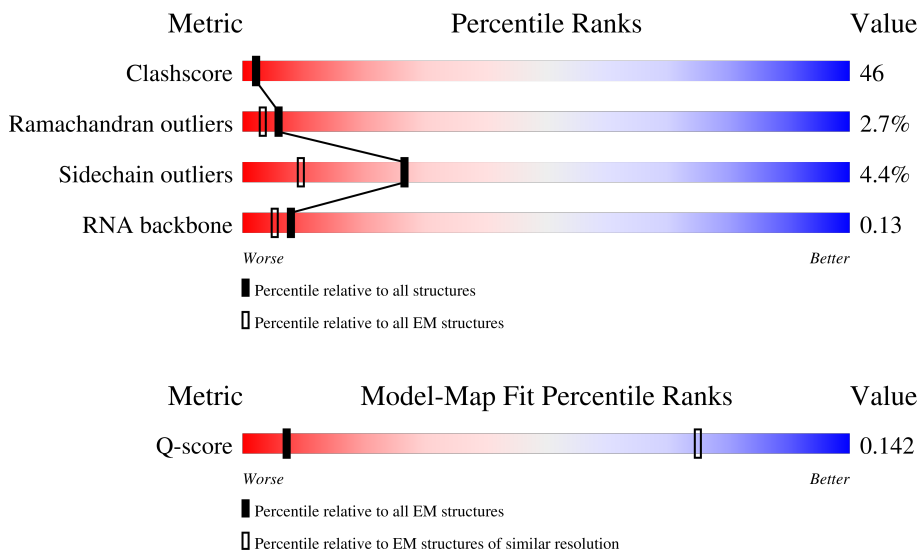
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 9.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	258 (8.40 - 9.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	
2	B	403	
3	C	427	

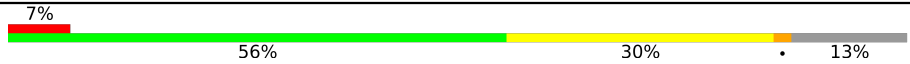

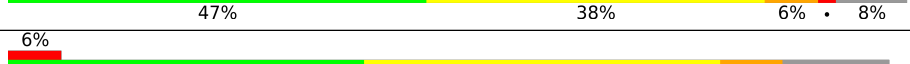
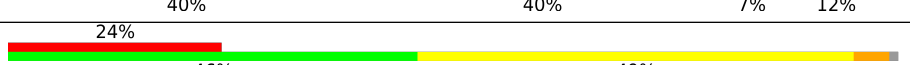
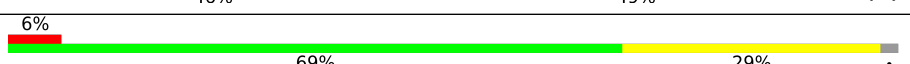
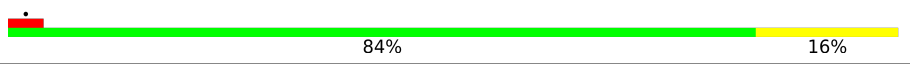

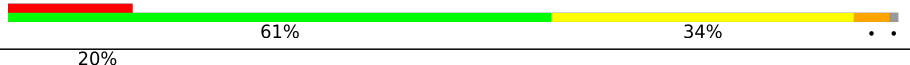
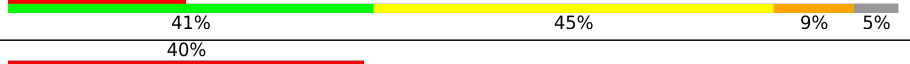
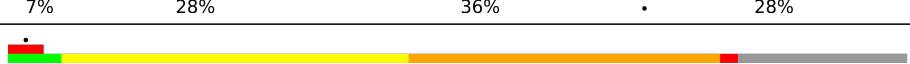



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Mol	Chain	Length	Quality of chain
4	D	297	15% 53% 41% . .
5	E	288	15% 21% 28% 6% . 45%
6	F	248	12% 50% 39% . 6%
7	G	266	17% 47% 34% 6% . 12%
8	H	192	9% 54% 42% . .
9	I	214	14% 51% 36% 5% 8%
10	J	178	10% 45% 39% 11% .
11	L	211	20% 44% 41% 9% . 5%
12	M	215	11% 30% 33% . 35%
13	N	204	15% 56% 42% .
14	O	203	10% 50% 41% 5% .
15	P	184	10% 41% 36% 5% 17%
16	Q	188	19% 49% 41% 7% .
17	R	196	15% 54% 34% 6% . 7%
18	S	176	13% 50% 41% 6% . .
19	T	160	19% 51% 43% 5% . .
20	U	128	13% 51% 26% . 20%
21	V	140	19% 61% 29% . 9%
22	W	157	5% 27% 10% . 59%
23	X	156	16% 44% 32% . 24%
24	Y	145	8% 41% 41% 6% 12%
25	Z	136	18% 49% 46% . .
26	a	148	16% 52% 43% . .
27	b	159	8% 25% 15% . 57%
28	c	115	17% 46% 41% . 10%

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Mol	Chain	Length	Quality of chain
29	d	125	
30	e	135	
31	f	110	
32	g	117	
33	h	123	
34	i	105	
35	j	97	
36	k	70	
37	l	51	
38	m	128	
39	n	25	
40	o	106	
41	p	92	
42	t	137	
43	u	210	
44	2	5025	
45	3	194	
46	4	121	

2 Entry composition [i](#)

There are 46 unique types of molecules in this entry. The entry contains 136495 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	247	1888	1183	388	311	6	0	1

- Molecule 2 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	396	3190	2030	601	545	14	0	1

- Molecule 3 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	364	2889	1817	578	480	14	0	1

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	290	2361	1489	431	427	14	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	E	158	1286	834	238	214	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	234	1949	1252	376	312	9	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	G	235	1881	1197	363	317	4	0	1

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	H	192	1535	965	286	278	6	0	0

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	I	196	1604	1022	308	262	12	0	0

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	J	170	1362	861	254	241	6	0	0

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	200	1617	1013	335	265	4	0	1

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	140	1139	730	219	183	7	0	1

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	N	204	1708	1077	360	266	5	0	0

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	196	Total	C	N	O	S	0	1
			1607	1034	316	252	5		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	153	Total	C	N	O	S	0	1
			1234	771	241	213	9		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	184	Total	C	N	O	S	0	0
			1493	933	311	244	5		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	183	Total	C	N	O	S	0	1
			1526	943	331	242	10		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	173	Total	C	N	O	S	0	0
			1438	916	280	232	10		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	159	Total	C	N	O	S	0	0
			1297	823	252	216	6		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	102	Total	C	N	O	S	0	1
			827	529	146	150	2		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	V	128	Total	C	N	O	S	0	0
			963	610	181	167	5		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	W	64	Total	C	N	O	S	0	1
			529	337	104	85	3		

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	X	119	Total	C	N	O	S	0	0
			975	624	183	167	1		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Y	128	Total	C	N	O	S	0	1
			1065	668	217	177	3		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Z	136	Total	C	N	O	S	0	0
			1114	719	209	182	4		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	147	Total	C	N	O	S	0	0
			1161	736	237	185	3		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	69	Total	C	N	O	S	0	1
			560	344	123	90	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	104	802	508	142	145	7	0	1

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	d	109	904	570	174	158	2	0	0

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	e	128	1053	664	219	165	5	0	1

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	f	107	865	550	172	140	3	0	0

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	g	115	907	566	188	147	6	0	1

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	h	122	1014	641	205	167	1	0	0

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	i	97	783	488	168	122	5	0	1

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	j	85	Total	C	N	O	S	0	1
			690	423	153	109	5		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			568	366	103	98	1		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	l	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 38 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	m	52	Total	C	N	O	S	0	0
			428	266	90	66	6		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	o	106	Total	C	N	O	S	0	0
			870	547	176	140	7		

- Molecule 41 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	p	91	Total	C	N	O	S	0	0
			707	445	136	119	7		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	t	130	1043	646	220	172	5	0	1

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	u	210	1621	990	278	347	6	0	0

- Molecule 44 is a RNA chain called 28S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
44	2	3616	77488	34508	14153	25212	3615	0	0

- Molecule 45 is a RNA chain called 5.8S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	3	157	3334	1489	587	1102	156	0	0

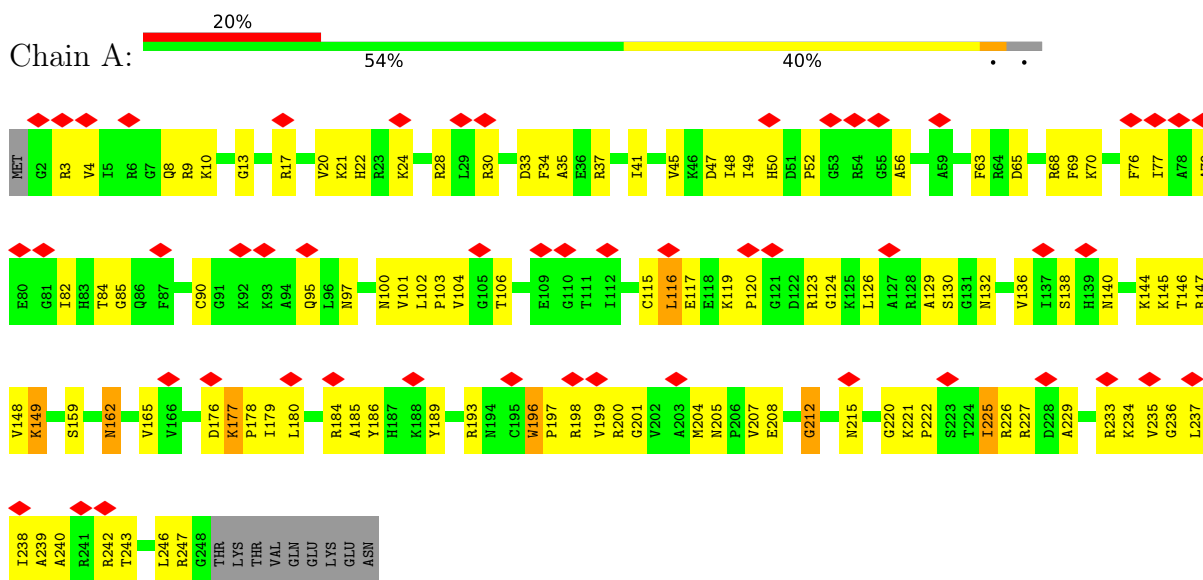
- Molecule 46 is a RNA chain called 5S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
46	4	119	2538	1132	454	834	118	0	0

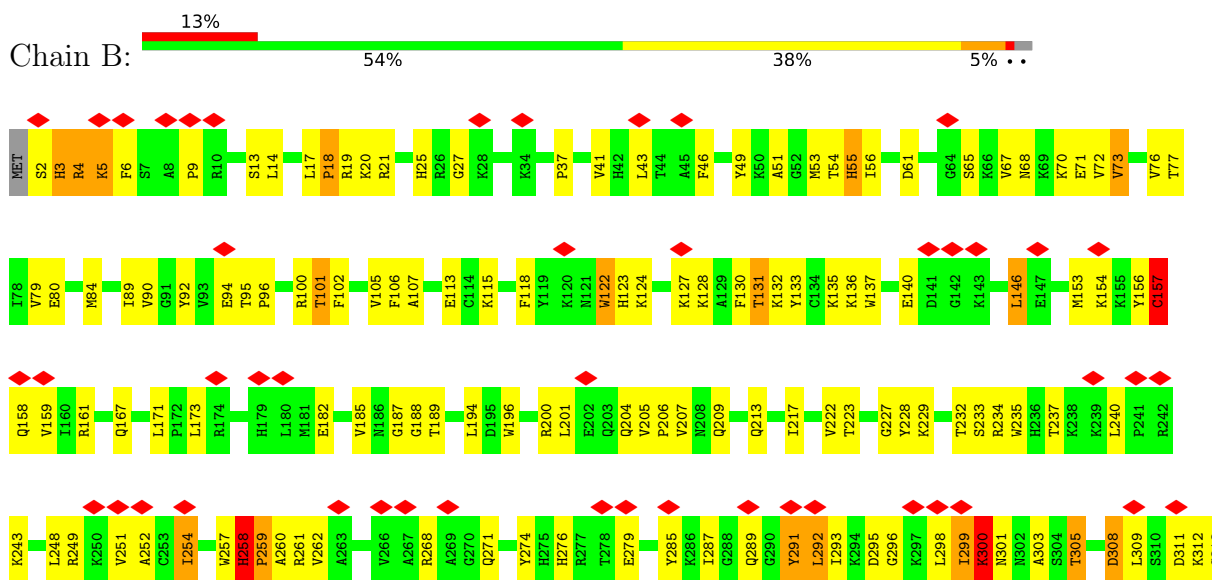
3 Residue-property plots

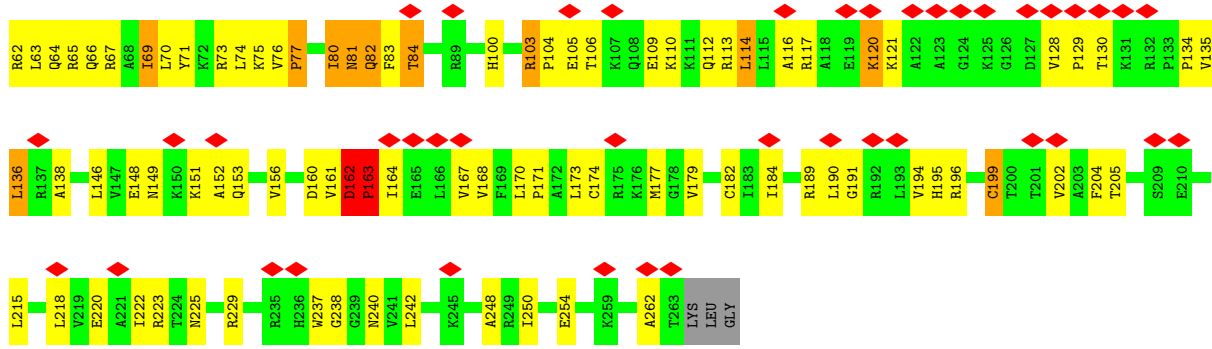
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 60S RIBOSOMAL PROTEIN L8

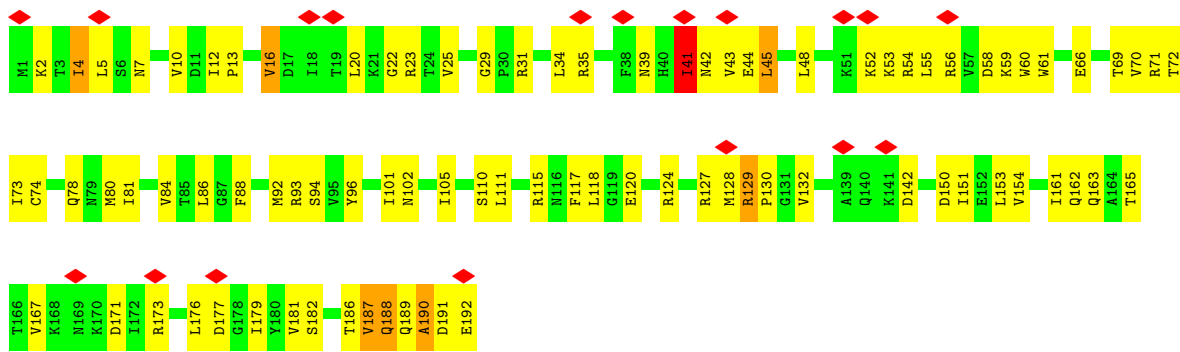


• Molecule 2: 60S RIBOSOMAL PROTEIN L3

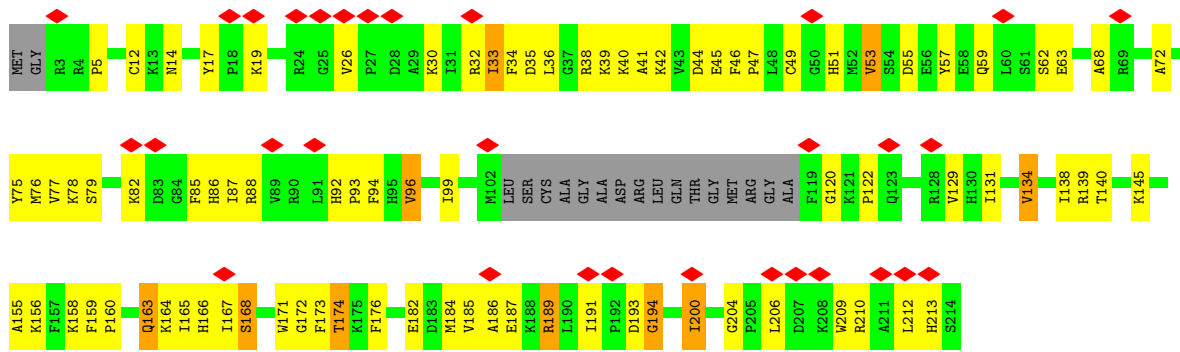




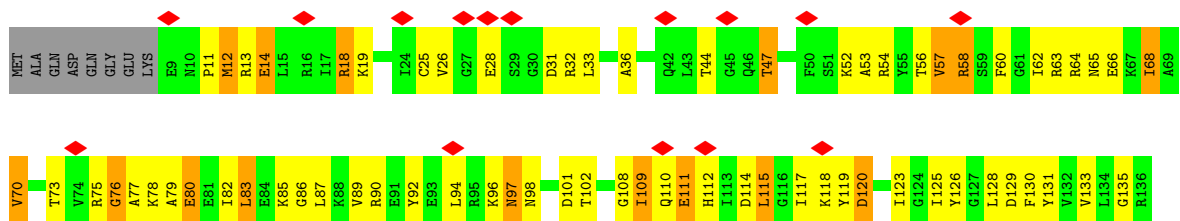
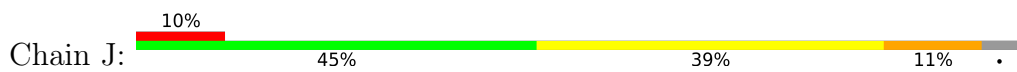
• Molecule 8: 60S RIBOSOMAL PROTEIN L9

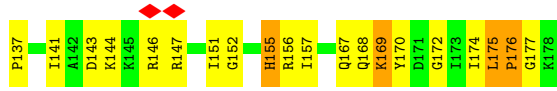


• Molecule 9: 60S RIBOSOMAL PROTEIN L10

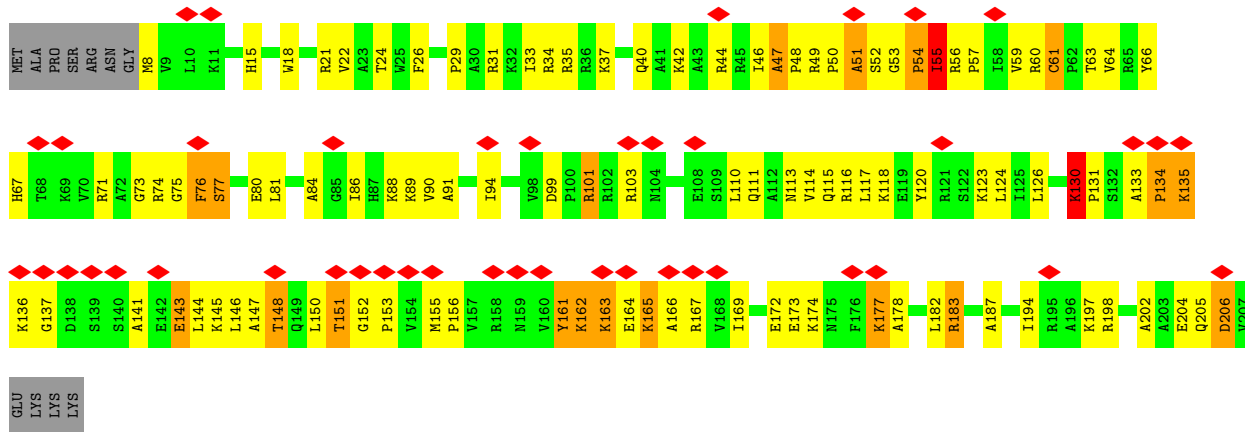
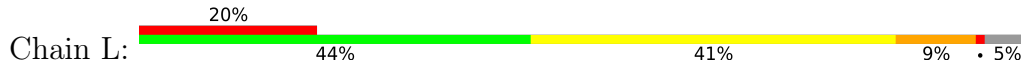


• Molecule 10: 60S RIBOSOMAL PROTEIN L11

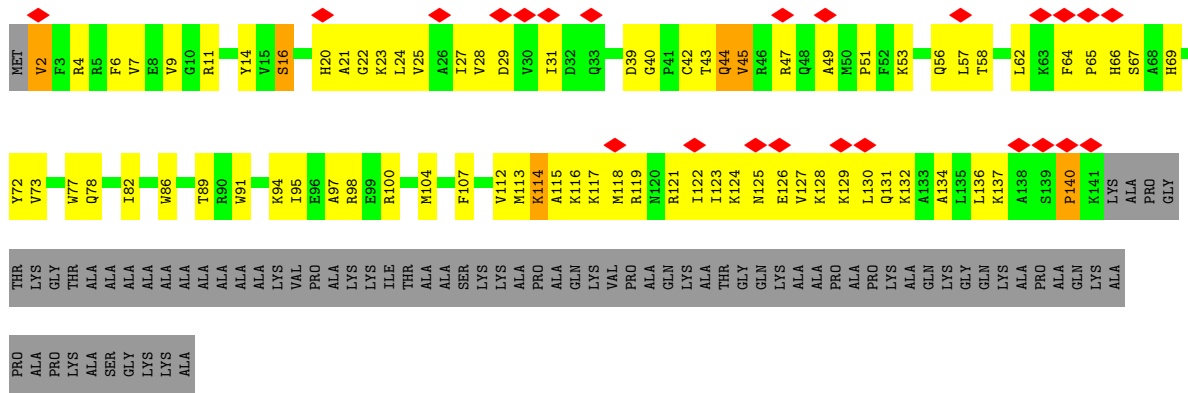
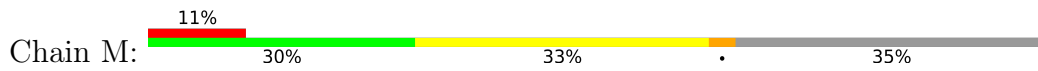




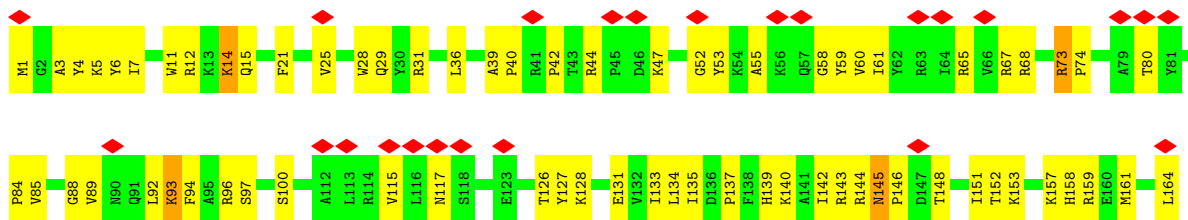
• Molecule 11: 60S RIBOSOMAL PROTEIN L13

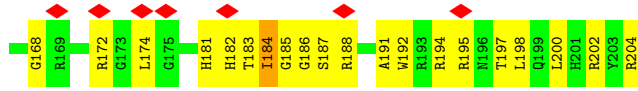


• Molecule 12: 60S RIBOSOMAL PROTEIN L14

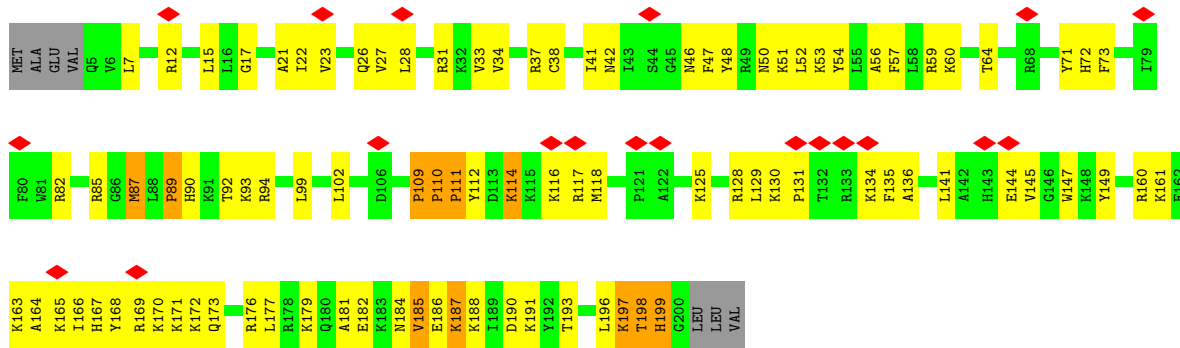


• Molecule 13: 60S RIBOSOMAL PROTEIN L15

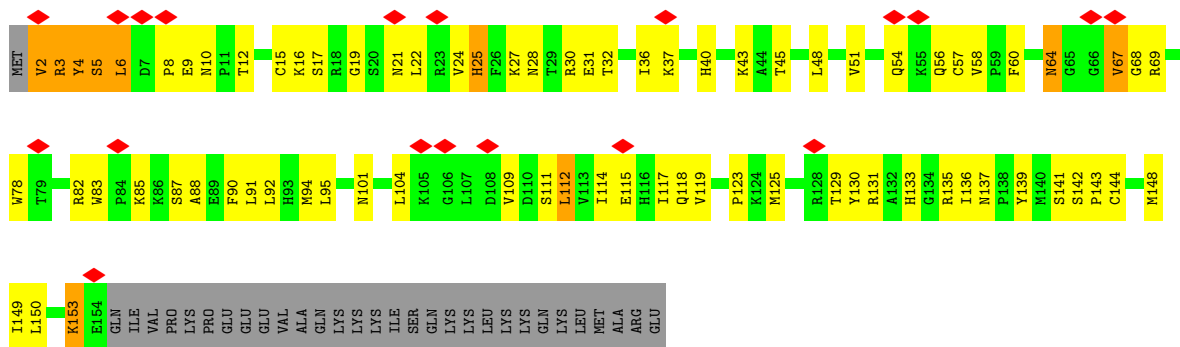




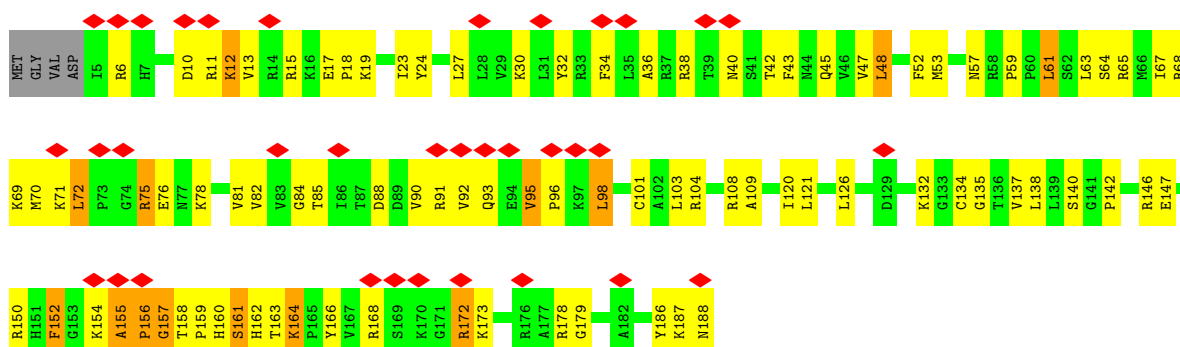
• Molecule 14: 60S RIBOSOMAL PROTEIN L13A



• Molecule 15: 60S RIBOSOMAL PROTEIN L17

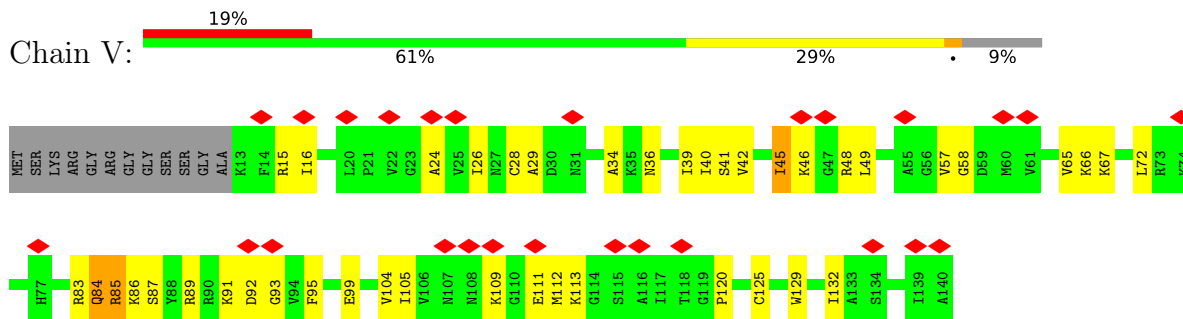


• Molecule 16: 60S RIBOSOMAL PROTEIN L18

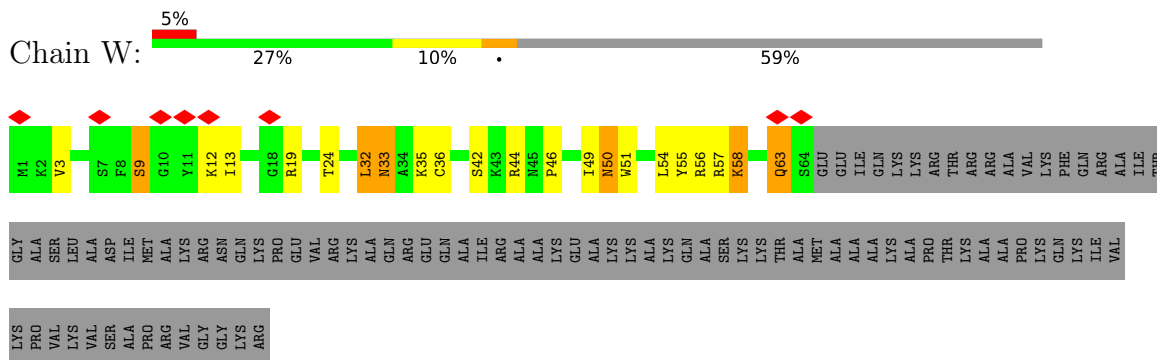


• Molecule 17: 60S RIBOSOMAL PROTEIN L19

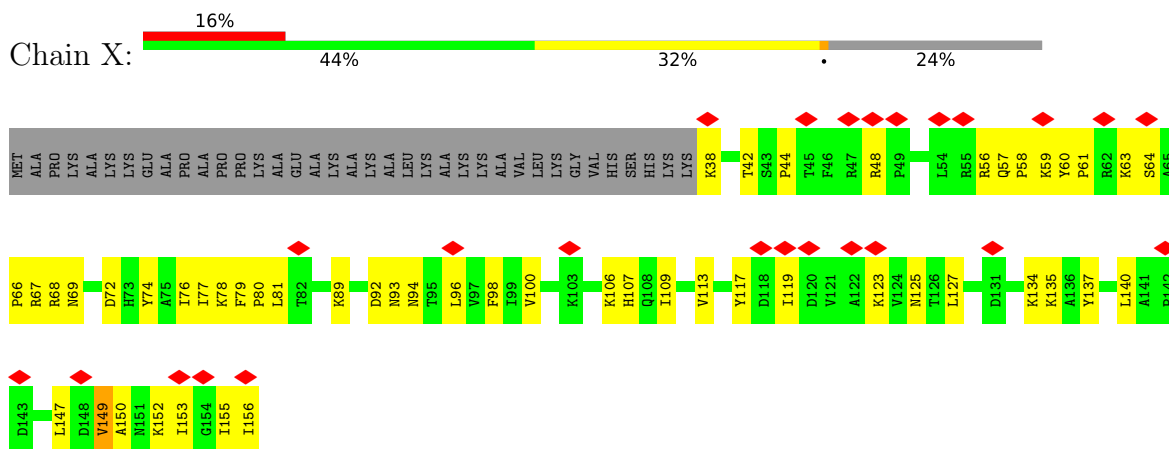
• Molecule 21: 60S RIBOSOMAL PROTEIN L23



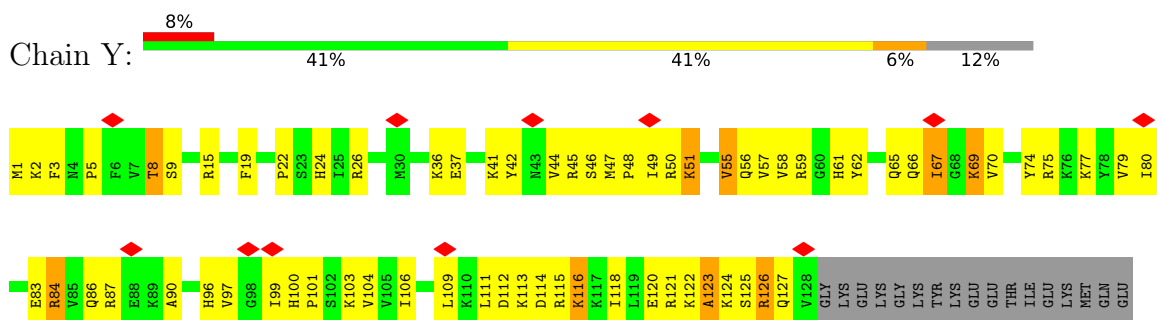
• Molecule 22: 60S RIBOSOMAL PROTEIN L24



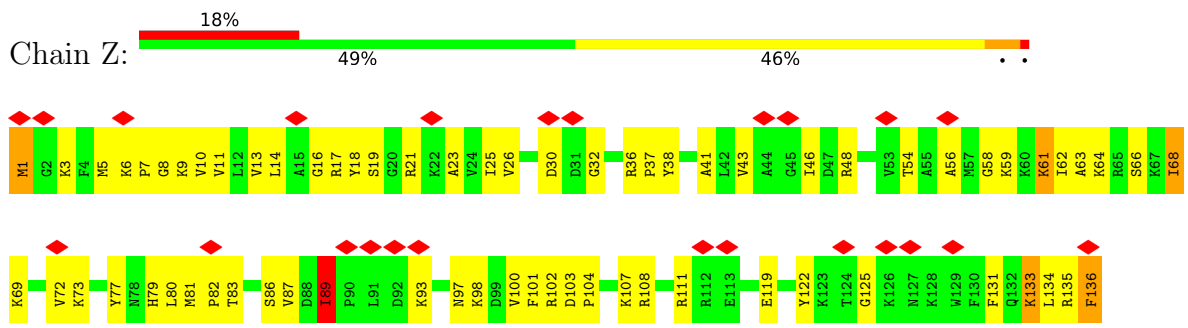
• Molecule 23: 60S RIBOSOMAL PROTEIN L23A



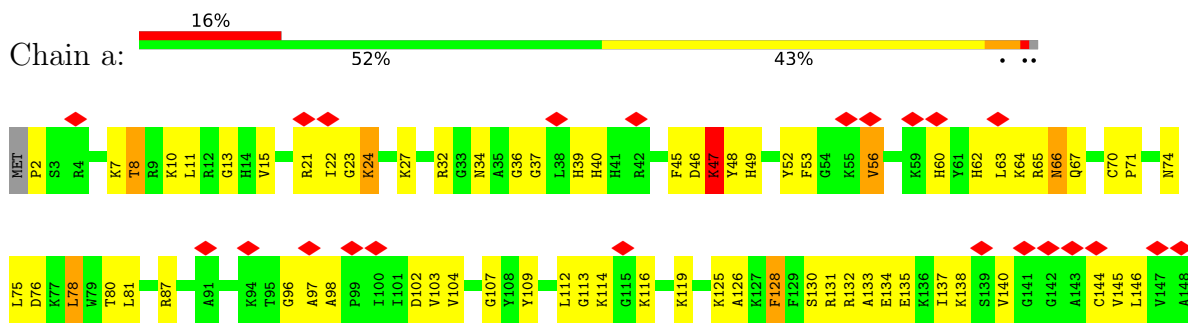
• Molecule 24: 60S RIBOSOMAL PROTEIN L26



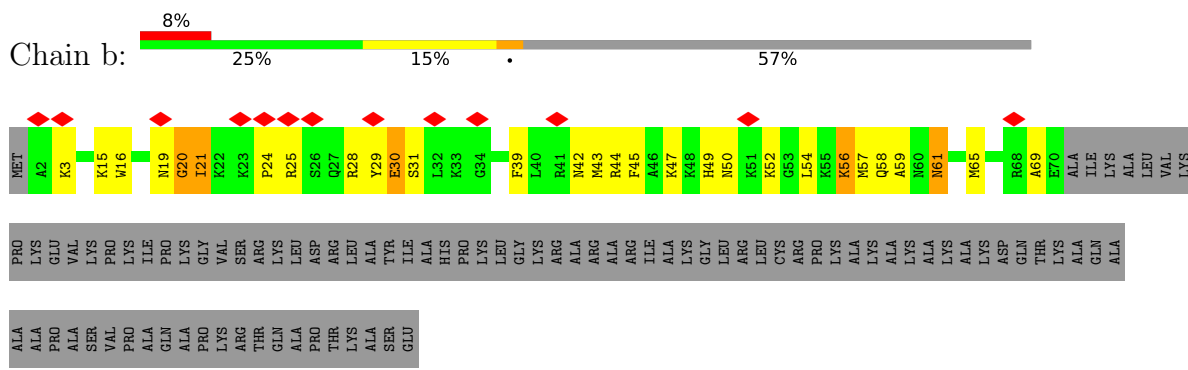
• Molecule 25: 60S RIBOSOMAL PROTEIN L27



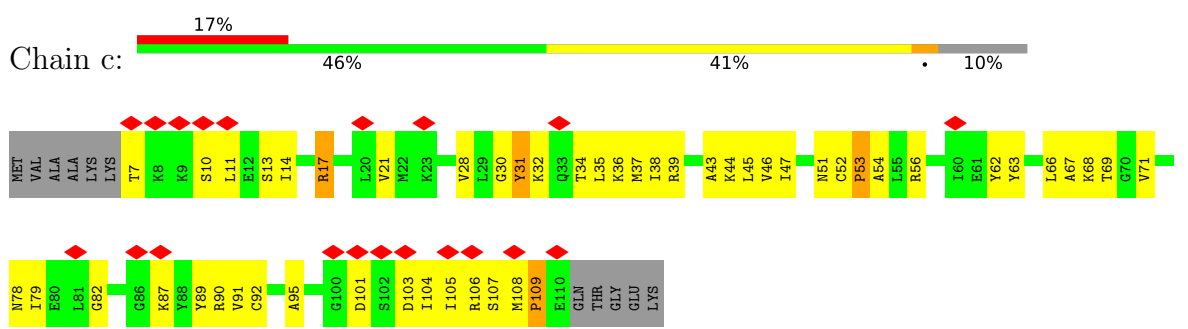
• Molecule 26: 60S RIBOSOMAL PROTEIN L27A



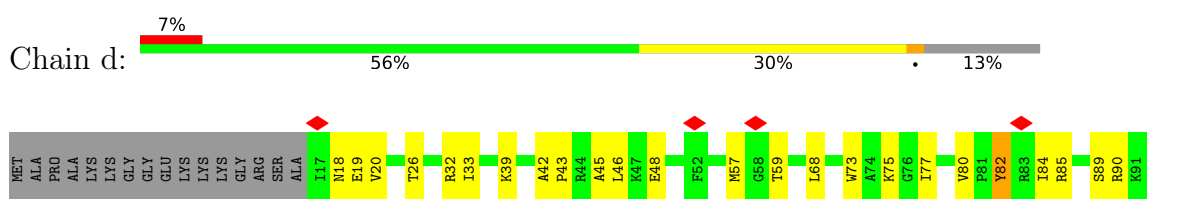
• Molecule 27: 60S RIBOSOMAL PROTEIN L29



• Molecule 28: 60S RIBOSOMAL PROTEIN L30

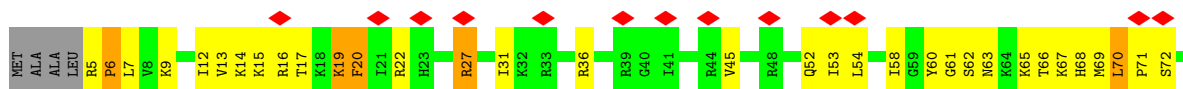


• Molecule 29: 60S RIBOSOMAL PROTEIN L31

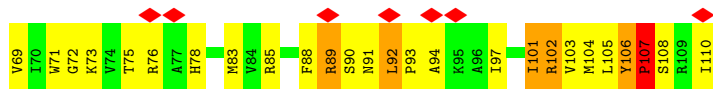




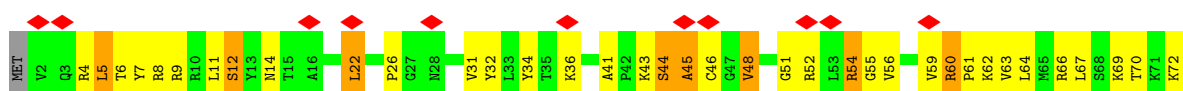
• Molecule 30: 60S RIBOSOMAL PROTEIN L32



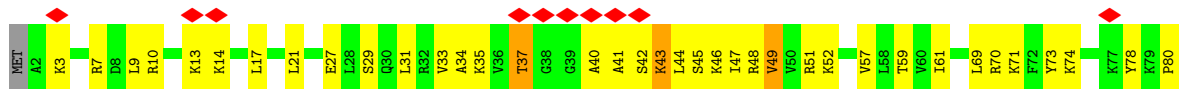
• Molecule 31: 60S RIBOSOMAL PROTEIN L35A



• Molecule 32: 60S RIBOSOMAL PROTEIN L34

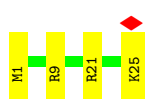
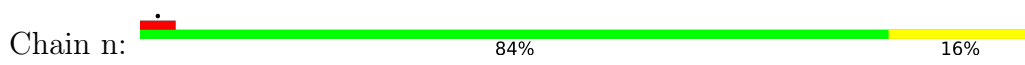


• Molecule 33: 60S RIBOSOMAL PROTEIN L35

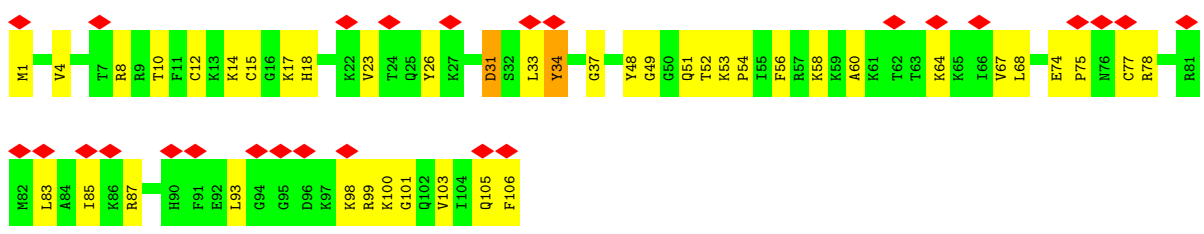


• Molecule 34: 60S RIBOSOMAL PROTEIN L36

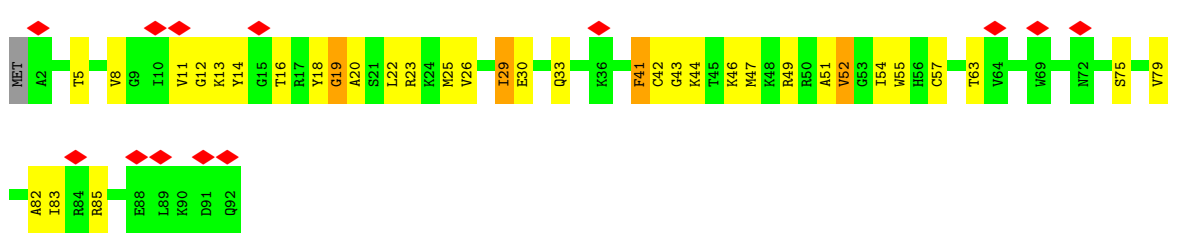




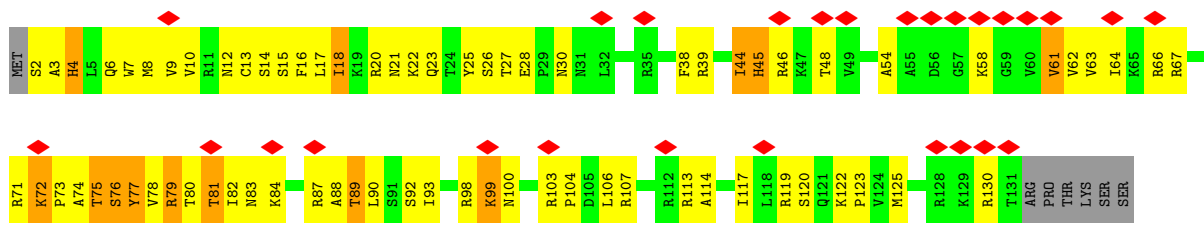
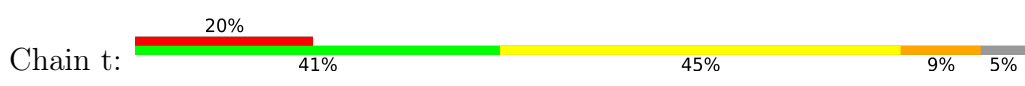
• Molecule 40: 60S RIBOSOMAL PROTEIN L36A



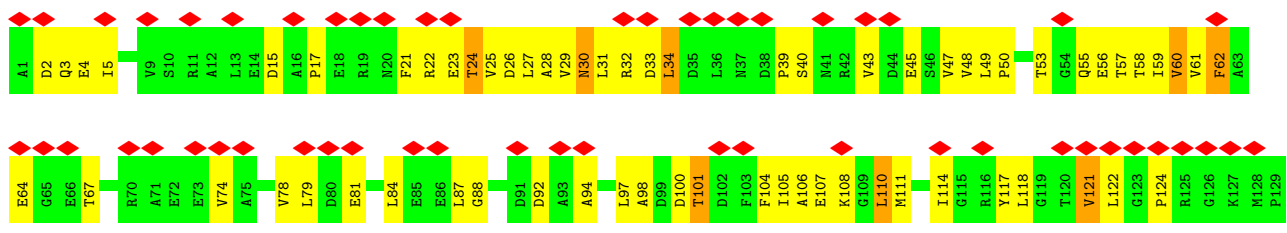
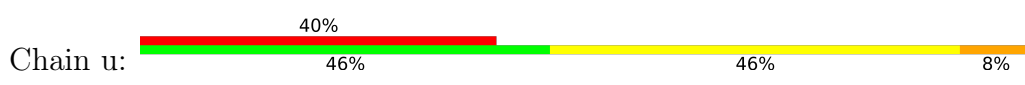
• Molecule 41: 60S RIBOSOMAL PROTEIN L37A

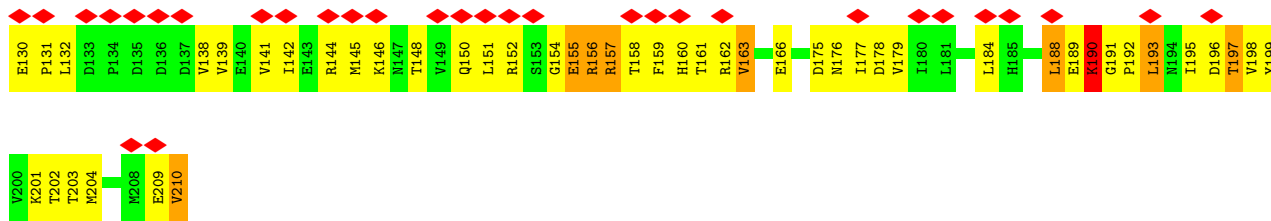


• Molecule 42: 60S RIBOSOMAL PROTEIN L28

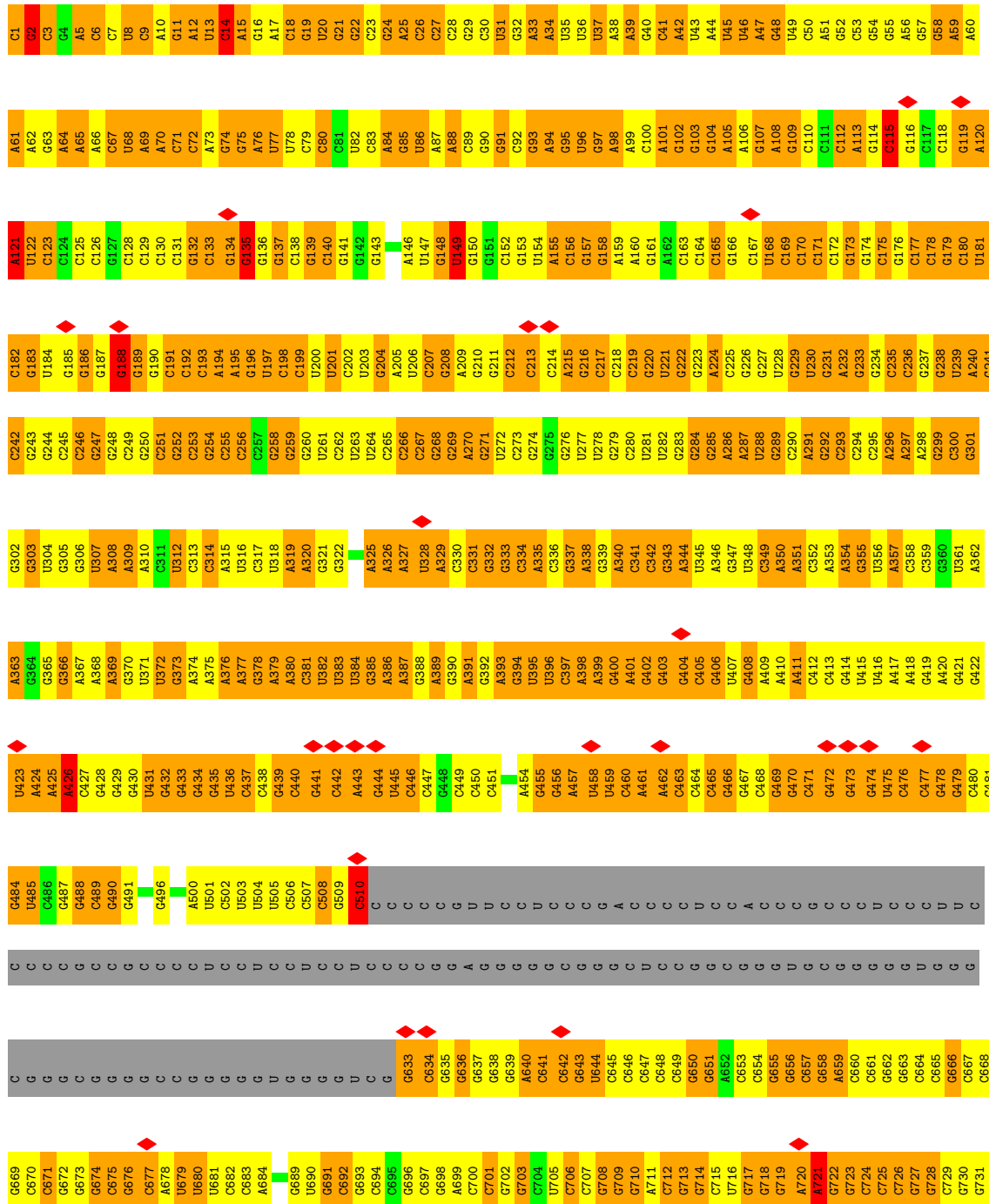


• Molecule 43: 60S RIBOSOMAL PROTEIN L10A

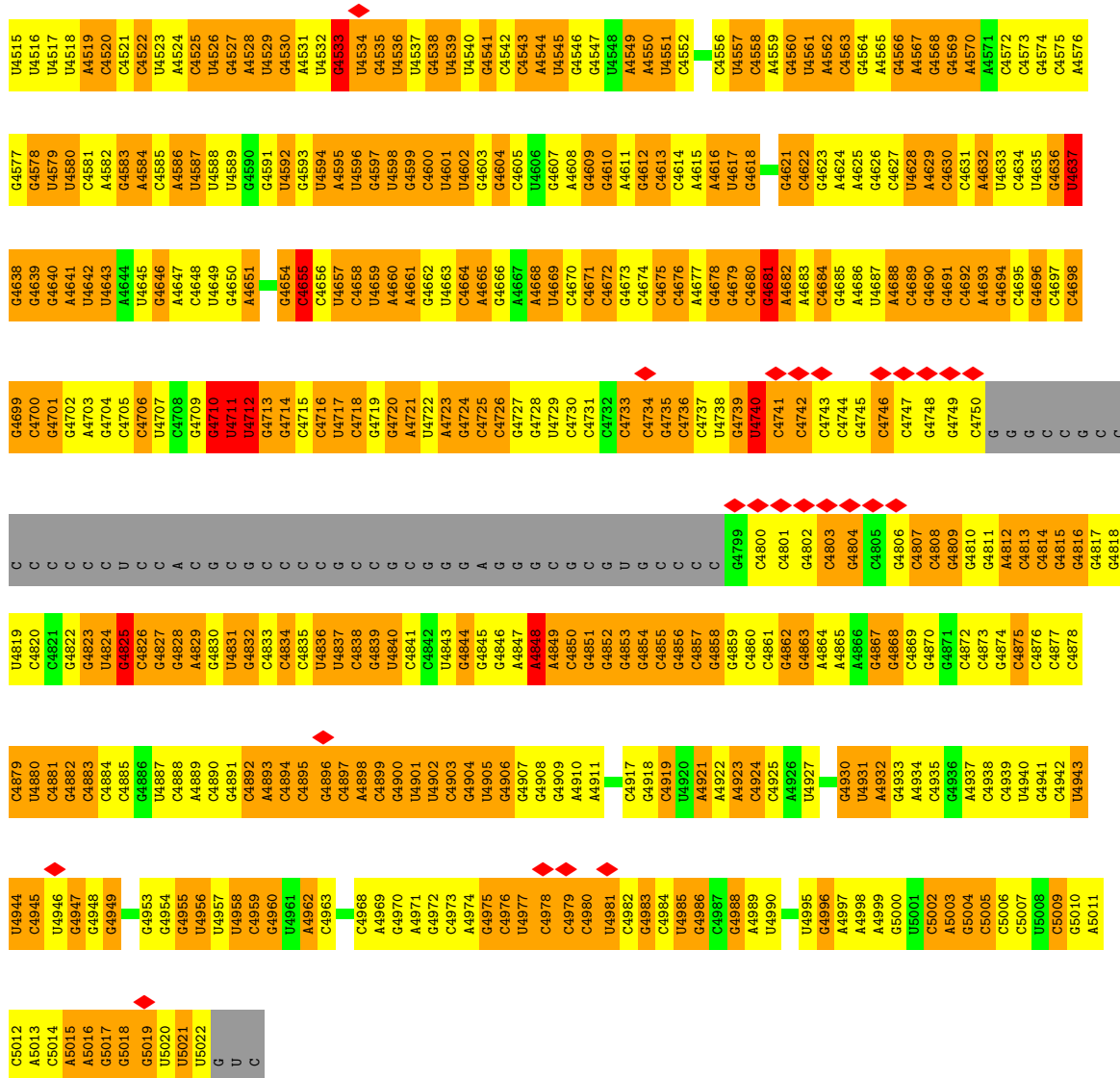




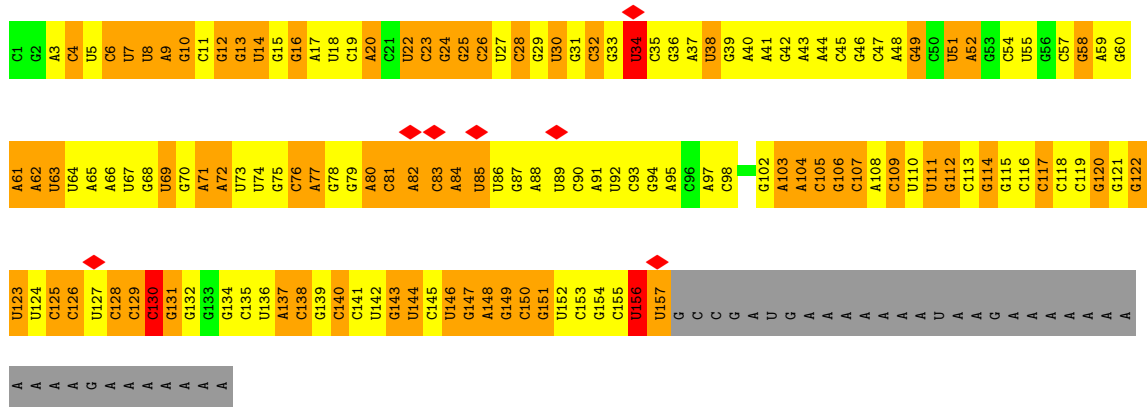
• Molecule 44: 28S RRNA




U4453	G4393	G4383	U4272	G4147	U4084	U4023	C3900	C3839	A3776	A3716	C3653
G4454	C4394	U4334	A4273	U4148	U4085	A4024	G3903	A3840	C3777	A3717	C3654
A4455	U4395	C4335	G4276	U4149	C4086	C4025	C3904	A3841	G3778	C3718	C3655
U4457	U4396	A4336	A4277	U4150	C4087	U4026	G3905	G3842	C3779	C3719	A3656
G4459	U4397	A4337	A4278	A4152	G4088	U4027	C3906	G3843	G3780	G3720	U3657
U4460	U4398	A4338	C4279	C4153	C4089	A4028	G3907	G3844	C3781	C3721	G3658
U4461	G4400	A4340	U4280	U4154	G4090	G4029	G3908	A3845	A3782	G3722	U3659
G4465	A4401	A4341	U4281	G4155	U4091	U4030	G3909	A3846	G3783	G3723	G3660
U4466	U4402	G4342	G4282	G4156	C4092	A4031	G3910	C3847	G3784	G3724	A3661
G4467	C4403	U4343	C4283	C4157	C4093	C4032	A3911	G3848	A3785	A3725	U3662
U4472	C4404	U4344	A4284	G4158	A4094	U4033	A3912	G3849	A3786	G3726	U3663
A4473	U4405	A4345	C4285	C4159	A4095	U4034	G3913	G3850	U3787	U3727	U3664
G4474	U4406	C4346	G4286	G4160	G4096	U4035	A3914	C3851	G3788	A3728	C3665
U4469	C4407	C4347	U4287	G4161	G4098	U4036	A3915	U3852	G3789	U3666	U3666
A4470	G4408	A4348	G4288	U4162	C4099	U4037	G3916	A3853	A3790	C3730	C3667
U4471	A4409	A4349	A4289	A4163	C4100	U4038	U3919	G3854	U3791	U3731	C3668
A4472	U4410	U4350	G4290	C4164	A4101	U4039	G3920	C3855	A3792	A3732	C3669
A4473	G4411	A4351	A4291	A4165	G4102	C4040	A3921	G3856	G3793	U3733	C3670
G4474	U4412	G4352	C4292	C4166	C4103	A4041	G3922	G3857	G3794	G3734	A3671
U4465	C4413	G4353	C4293	C4167	A4104	C4042	A3923	A3858	A3795	A3735	G3672
G4476	U4414	A4354	U4294	U4168	U4105	U4043	A3924	A3859	C3796	C3736	U3673
A4477	G4415	U4355	C4295	G4169	G4106	G4044	G3925	A3860	G3798	U3737	G3674
U4478	C4416	A4356	A4296	U4170	A4107	A4045	C3926	G3861	A3799	C3738	C3675
A4479	U4417	A4357	C4297	U4171	C4108	C4046	U3926	G3862	U3800	U3739	U3676
G4480	C4418	C4358	G4298	A4173	C4109	C4047	U3927	A3863	U3801	C3740	C3677
U4481	U4419	U4359	A4299	A4174	G4110	C4048	U3928	G3864	C3802	U3741	U3678
G4482	U4420	G4360	C4299	A4175	A4111	G4050	A3929	G3865	C3803	U3742	U3679
A4483	C4421	C4361	A4299	G4176	G4112	U4051	G3930	G3866	G3804	U3743	A3680
G4484	C4422	C4362	C4240	C4177	C4113	U4052	A3931	G3867	A3805	A3744	A3681
C4485	U4423	U4363	A4241	U4178	G4114	A4053	A3932	A3870	G3806	G3745	U3682
U4486	A4424	U4364	A4242	A4179	A4117	G4054	U3933	A3871	U3807	G3746	G3683
G4487	U4425	G4365	U4243	A4180	C4118	C4055	U3934	A3872	C3808	U3747	U3684
U4488	C4426	U4366	U4244	C4181	C4119	C4056	A3935	A3873	U3809	A3748	U3685
A4489	A4427	G4367	G4307	G4182	C4120	G4057	G3936	G3874	C3810	C3750	A3686
U4490	U4428	G4368	C4247	C4183	G4121	U4058	U3937	A3875	C3811	A3751	A3687
U4491	U4429	C4369	C4248	A4184	C4122	G4059	G3938	G3876	C3812	C3752	A3688
U4492	G4430	G4370	U4249	G4185	U4123	G4060	C3940	A3877	A3815	A3753	G3689
A4493	U4431	G4371	U4250	C4186	C4124	G4061	A3941	C3878	C3815	A3754	C3691
G4494	C4432	C4372	G4251	U4187	C4125	G4062	G3942	C3879	U3755	U3755	A3692
A4495	A4433	C4373	A4252	G4188	G4126	G4063	G3943	C3880	G3756	G3756	A3693
C4496	A4434	A4374	U4253	U4189	G4127	C4064	C3944	U3881	U3820	C3757	G3694
G4497	G4435	A4375	C4254	C4190	G4128	G4065	C3945	G3882	C3758	C3758	A3695
U4498	C4436	G4376	U4255	C4191	G4129	A4066	C3946	U3883	U3759	A3696	A3696
U4499	A4437	C4377	U4256	U4192	A4130	G4067	G4007	U3884	C3760	A3697	A3697
C4500	G4438	G4378	G4257	A4193	C4131	C4068	C4008	G3885	G3761	C3761	U3698
G4501	A4439	U4379	A4258	A4194	A4132	C4069	C4009	A3886	G3762	U3762	U3699
U4502	U4440	U4380	U4259	G4195	G4133	C4070	G4010	G3887	C3763	C3763	C3700
G4503	U4441	C4381	U4260	U4196	U4134	C4071	G4011	C3888	C3764	A3764	G3701
A4504	U4442	A4382	U4261	C4197	G4135	G4072	U4012	U3889	U3765	U3765	A3702
G4505	G4443	U4383	U4262	C4198	C4136	A4073	G4013	U3890	C3766	C3766	U3703
A4506	C4444	A4384	C4263	A4199	A4137	G4074	A4014	G3891	U3767	U3767	G3704
U4507	U4445	C4385	A4264	G4200	A4138	A4075	A4015	A3892	A3768	A3768	A3705
A4508	C4446	C4386	G4265	C4201	G4139	C4076	A4016	C3893	A3769	A3769	A3706
G4509	U4447	G4387	U4266	U4141	U4140	C4077	U4017	G3894	C3832	C3832	A3707
U4510	A4448	C4388	C4267	U4142	C4078	U4078	C4018	C3895	C3833	U3770	U3770
A4511	G4449	C4389	A4268	A4204	A4141	U4079	C4019	U3896	C3834	U3771	C3710
U4512	C4450	G4390	G4269	G4143	G4143	A4080	C4020	A3897	A3836	A3772	C3711
A4513	U4451	U4391	A4270	G4144	A4144	U4081	A4021	G3898	G3837	U3773	U3714
G4514	U4452	C4392	A4271	A4146	A4146	C4083	C4022	U3899	C3838	G3775	A3715

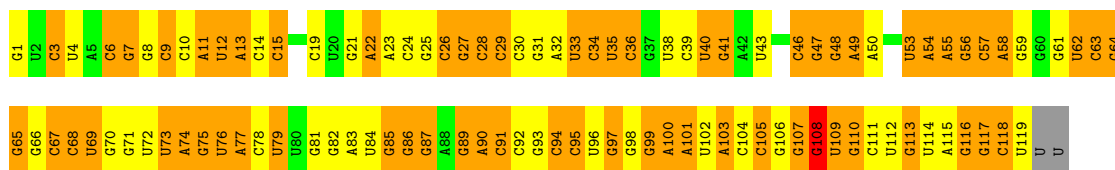


• Molecule 45: 5.8S RRNA



• Molecule 46: 5S RRNA

Chain 4:  12% 33% 52% ..



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	64902	Depositor
Resolution determination method	Not provided	
CTF correction method	DEFOCUS GROUPS	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	194805	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	12.165	Depositor
Minimum map value	-4.363	Depositor
Average map value	0.164	Depositor
Map value standard deviation	0.954	Depositor
Recommended contour level	3	Depositor
Map size (\AA)	467.99997, 467.99997, 467.99997	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.56, 1.56, 1.56	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.68	1/1926 (0.1%)	1.09	3/2583 (0.1%)
2	B	0.72	2/3258 (0.1%)	1.12	10/4361 (0.2%)
3	C	0.76	1/2943 (0.0%)	1.16	16/3953 (0.4%)
4	D	0.78	6/2406 (0.2%)	1.12	12/3221 (0.4%)
5	E	0.82	1/1311 (0.1%)	1.17	8/1763 (0.5%)
6	F	0.68	0/1985	1.12	10/2644 (0.4%)
7	G	0.75	1/1914 (0.1%)	1.20	14/2578 (0.5%)
8	H	0.64	0/1554	1.10	4/2089 (0.2%)
9	I	0.68	0/1642	1.15	13/2194 (0.6%)
10	J	0.79	0/1385	1.18	9/1852 (0.5%)
11	L	0.82	6/1647 (0.4%)	1.18	14/2205 (0.6%)
12	M	0.79	1/1162 (0.1%)	1.12	1/1556 (0.1%)
13	N	0.69	0/1753	1.07	10/2348 (0.4%)
14	O	0.72	2/1639 (0.1%)	1.15	11/2193 (0.5%)
15	P	0.67	1/1260 (0.1%)	1.09	2/1691 (0.1%)
16	Q	0.71	0/1517	1.15	8/2026 (0.4%)
17	R	0.67	1/1542 (0.1%)	1.08	6/2037 (0.3%)
18	S	0.71	0/1478	1.19	14/1985 (0.7%)
19	T	0.74	0/1325	1.21	14/1770 (0.8%)
20	U	0.74	1/841 (0.1%)	1.16	8/1128 (0.7%)
21	V	0.69	1/977 (0.1%)	1.03	0/1312
22	W	0.64	1/542 (0.2%)	0.98	2/722 (0.3%)
23	X	0.65	0/992	1.12	3/1334 (0.2%)
24	Y	0.74	1/1082 (0.1%)	1.18	5/1441 (0.3%)
25	Z	0.74	0/1137	1.25	5/1517 (0.3%)
26	a	0.72	0/1190	1.11	4/1591 (0.3%)
27	b	0.72	1/570 (0.2%)	1.10	1/752 (0.1%)
28	c	0.71	1/813 (0.1%)	1.05	3/1091 (0.3%)
29	d	0.70	0/919	1.06	2/1238 (0.2%)
30	e	0.71	1/1071 (0.1%)	1.12	5/1428 (0.4%)
31	f	0.75	1/884 (0.1%)	1.22	10/1185 (0.8%)
32	g	0.74	1/917 (0.1%)	1.15	4/1222 (0.3%)
33	h	0.64	0/1022	1.03	1/1351 (0.1%)
34	i	0.70	1/793 (0.1%)	1.18	6/1048 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	j	0.77	1/704 (0.1%)	1.16	4/931 (0.4%)
36	k	0.72	0/574	1.18	4/761 (0.5%)
37	l	0.65	0/453	1.04	2/599 (0.3%)
38	m	0.68	0/434	1.22	3/575 (0.5%)
39	n	0.62	0/240	0.86	0/305
40	o	0.70	0/884	1.14	4/1166 (0.3%)
41	p	0.64	0/717	0.97	1/953 (0.1%)
42	t	0.78	1/1058 (0.1%)	1.22	8/1416 (0.6%)
43	u	0.69	0/1638	1.12	6/2222 (0.3%)
44	2	0.34	12/86672 (0.0%)	0.66	30/135198 (0.0%)
45	3	0.30	0/3723	0.63	2/5800 (0.0%)
46	4	0.31	0/2836	0.67	1/4421 (0.0%)
All	All	0.51	47/147330 (0.0%)	0.85	303/217756 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
44	2	0	34
45	3	0	2
All	All	0	36

The worst 5 of 47 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	2	1701	C	O5'-C5'	16.69	1.67	1.42
44	2	1701	C	C5'-C4'	14.73	1.73	1.51
44	2	1673	C	C3'-O3'	13.64	1.63	1.43
44	2	1673	C	O3'-P	11.35	1.78	1.61
44	2	1673	C	O5'-C5'	10.39	1.58	1.42

The worst 5 of 303 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	2	1701	C	C2'-C3'-O3'	-18.40	86.10	113.70
44	2	1701	C	C4'-C3'-O3'	16.27	137.41	113.00
44	2	1701	C	O4'-C4'-C3'	-15.18	88.82	104.00
2	B	325	GLU	N-CA-C	12.18	124.63	111.36
44	2	1673	C	C4'-C3'-O3'	10.52	125.19	109.40

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	2	1	C	Sidechain
44	2	115	C	Sidechain
44	2	121	A	Sidechain
44	2	149	U	Sidechain
44	2	2	G	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1888	0	1983	144	0
2	B	3190	0	3327	169	0
3	C	2889	0	3064	307	0
4	D	2361	0	2385	159	0
5	E	1286	0	1398	180	0
6	F	1949	0	2093	133	0
7	G	1881	0	2018	143	0
8	H	1535	0	1611	95	0
9	I	1604	0	1652	61	0
10	J	1362	0	1399	92	0
11	L	1617	0	1725	140	0
12	M	1139	0	1204	123	0
13	N	1708	0	1761	105	0
14	O	1607	0	1745	121	0
15	P	1234	0	1263	89	0
16	Q	1493	0	1612	127	0
17	R	1526	0	1682	80	0
18	S	1438	0	1472	86	0
19	T	1297	0	1366	125	0
20	U	827	0	852	22	0
21	V	963	0	1026	44	0
22	W	529	0	541	27	0
23	X	975	0	1053	68	0
24	Y	1065	0	1145	103	0
25	Z	1114	0	1194	89	0
26	a	1161	0	1213	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
27	b	560	0	590	45	0
28	c	802	0	845	65	0
29	d	904	0	947	29	0
30	e	1053	0	1144	50	0
31	f	865	0	904	104	0
32	g	907	0	1002	105	0
33	h	1014	0	1148	55	0
34	i	783	0	862	77	0
35	j	690	0	719	61	0
36	k	568	0	637	40	0
37	l	443	0	483	19	0
38	m	428	0	466	25	0
39	n	239	0	289	3	0
40	o	870	0	943	51	0
41	p	707	0	760	39	0
42	t	1043	0	1120	137	0
43	u	1621	0	1555	258	0
44	2	77488	0	39153	7886	0
45	3	3334	0	1693	326	0
46	4	2538	0	1286	274	0
All	All	136495	0	98330	10756	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 46.

The worst 5 of 10756 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:f:106:TYR:CD2	31:f:107:PRO:HD2	1.42	1.55
43:u:156:ARG:HG2	44:2:4023:U:C2	0.98	1.48
44:2:1673:C:O3'	44:2:1673:C:C3'	1.63	1.46
43:u:156:ARG:NE	44:2:3935:A:C2	1.72	1.44
34:i:100:ALA:CB	43:u:197:THR:OG1	1.69	1.39

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	245/257 (95%)	236 (96%)	6 (2%)	3 (1%)	10	44
2	B	394/403 (98%)	369 (94%)	11 (3%)	14 (4%)	2	20
3	C	362/427 (85%)	338 (93%)	9 (2%)	15 (4%)	2	18
4	D	288/297 (97%)	279 (97%)	4 (1%)	5 (2%)	7	36
5	E	156/288 (54%)	141 (90%)	8 (5%)	7 (4%)	2	17
6	F	232/248 (94%)	225 (97%)	3 (1%)	4 (2%)	7	36
7	G	233/266 (88%)	217 (93%)	7 (3%)	9 (4%)	2	19
8	H	190/192 (99%)	184 (97%)	3 (2%)	3 (2%)	7	38
9	I	192/214 (90%)	187 (97%)	2 (1%)	3 (2%)	7	38
10	J	168/178 (94%)	153 (91%)	3 (2%)	12 (7%)	1	11
11	L	198/211 (94%)	178 (90%)	9 (4%)	11 (6%)	1	14
12	M	138/215 (64%)	132 (96%)	4 (3%)	2 (1%)	9	40
13	N	202/204 (99%)	193 (96%)	6 (3%)	3 (2%)	8	40
14	O	194/203 (96%)	187 (96%)	4 (2%)	3 (2%)	8	40
15	P	151/184 (82%)	141 (93%)	7 (5%)	3 (2%)	6	31
16	Q	182/188 (97%)	169 (93%)	7 (4%)	6 (3%)	3	21
17	R	181/196 (92%)	174 (96%)	4 (2%)	3 (2%)	7	36
18	S	171/176 (97%)	158 (92%)	7 (4%)	6 (4%)	3	20
19	T	157/160 (98%)	150 (96%)	4 (2%)	3 (2%)	6	32
20	U	100/128 (78%)	97 (97%)	3 (3%)	0	100	100
21	V	126/140 (90%)	119 (94%)	5 (4%)	2 (2%)	7	38
22	W	62/157 (40%)	61 (98%)	1 (2%)	0	100	100
23	X	117/156 (75%)	113 (97%)	4 (3%)	0	100	100
24	Y	126/145 (87%)	119 (94%)	4 (3%)	3 (2%)	4	27
25	Z	134/136 (98%)	125 (93%)	5 (4%)	4 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	a	145/148 (98%)	134 (92%)	6 (4%)	5 (3%)	3	21
27	b	67/159 (42%)	60 (90%)	3 (4%)	4 (6%)	1	13
28	c	102/115 (89%)	99 (97%)	1 (1%)	2 (2%)	6	31
29	d	107/125 (86%)	103 (96%)	3 (3%)	1 (1%)	14	51
30	e	126/135 (93%)	117 (93%)	6 (5%)	3 (2%)	4	27
31	f	105/110 (96%)	96 (91%)	4 (4%)	5 (5%)	2	16
32	g	113/117 (97%)	103 (91%)	6 (5%)	4 (4%)	3	20
33	h	120/123 (98%)	112 (93%)	5 (4%)	3 (2%)	4	26
34	i	95/105 (90%)	85 (90%)	4 (4%)	6 (6%)	1	13
35	j	83/97 (86%)	75 (90%)	6 (7%)	2 (2%)	4	27
36	k	67/70 (96%)	64 (96%)	2 (3%)	1 (2%)	8	40
37	l	48/51 (94%)	46 (96%)	1 (2%)	1 (2%)	5	30
38	m	50/128 (39%)	48 (96%)	1 (2%)	1 (2%)	6	31
39	n	23/25 (92%)	23 (100%)	0	0	100	100
40	o	104/106 (98%)	98 (94%)	4 (4%)	2 (2%)	6	32
41	p	89/92 (97%)	83 (93%)	3 (3%)	3 (3%)	3	21
42	t	128/137 (93%)	112 (88%)	9 (7%)	7 (6%)	1	15
43	u	208/210 (99%)	199 (96%)	6 (3%)	3 (1%)	9	40
All	All	6479/7422 (87%)	6102 (94%)	200 (3%)	177 (3%)	6	25

5 of 177 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	196	TRP
2	B	4	ARG
2	B	5	LYS
2	B	157	CYS

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/199 (95%)	182 (96%)	7 (4%)	30	51
2	B	344/349 (99%)	322 (94%)	22 (6%)	16	37
3	C	302/348 (87%)	283 (94%)	19 (6%)	16	37
4	D	244/250 (98%)	237 (97%)	7 (3%)	37	58
5	E	143/252 (57%)	133 (93%)	10 (7%)	14	35
6	F	203/215 (94%)	195 (96%)	8 (4%)	28	49
7	G	199/223 (89%)	190 (96%)	9 (4%)	24	46
8	H	171/171 (100%)	165 (96%)	6 (4%)	32	53
9	I	170/181 (94%)	161 (95%)	9 (5%)	20	41
10	J	143/149 (96%)	137 (96%)	6 (4%)	26	48
11	L	167/177 (94%)	157 (94%)	10 (6%)	17	39
12	M	118/161 (73%)	113 (96%)	5 (4%)	26	48
13	N	172/172 (100%)	167 (97%)	5 (3%)	37	58
14	O	168/174 (97%)	165 (98%)	3 (2%)	51	68
15	P	133/163 (82%)	126 (95%)	7 (5%)	20	41
16	Q	162/165 (98%)	157 (97%)	5 (3%)	35	56
17	R	161/175 (92%)	151 (94%)	10 (6%)	16	38
18	S	155/157 (99%)	149 (96%)	6 (4%)	28	49
19	T	139/140 (99%)	135 (97%)	4 (3%)	37	58
20	U	91/115 (79%)	91 (100%)	0	100	100
21	V	100/107 (94%)	100 (100%)	0	100	100
22	W	55/126 (44%)	52 (94%)	3 (6%)	19	41
23	X	107/133 (80%)	105 (98%)	2 (2%)	50	67
24	Y	119/135 (88%)	114 (96%)	5 (4%)	26	48
25	Z	118/118 (100%)	114 (97%)	4 (3%)	32	54
26	a	120/121 (99%)	115 (96%)	5 (4%)	26	48
27	b	58/126 (46%)	57 (98%)	1 (2%)	53	69
28	c	88/97 (91%)	87 (99%)	1 (1%)	65	76
29	d	100/110 (91%)	97 (97%)	3 (3%)	36	57
30	e	115/121 (95%)	111 (96%)	4 (4%)	32	53
31	f	87/89 (98%)	77 (88%)	10 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	98/100 (98%)	89 (91%)	9 (9%)	8	27
33	h	109/110 (99%)	105 (96%)	4 (4%)	30	51
34	i	82/89 (92%)	76 (93%)	6 (7%)	13	34
35	j	71/80 (89%)	69 (97%)	2 (3%)	38	60
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	46 (98%)	1 (2%)	47	65
38	m	48/116 (41%)	45 (94%)	3 (6%)	16	37
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	94/94 (100%)	90 (96%)	4 (4%)	26	47
41	p	74/75 (99%)	72 (97%)	2 (3%)	39	61
42	t	113/121 (93%)	108 (96%)	5 (4%)	25	47
43	u	177/177 (100%)	161 (91%)	16 (9%)	9	27
All	All	5642/6318 (89%)	5394 (96%)	248 (4%)	27	47

5 of 248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	M	45	VAL
40	o	83	LEU
17	R	41	ILE
38	m	115	CYS
43	u	53	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
26	a	74	ASN
42	t	23	GLN
28	c	15	ASN
33	h	101	ASN
10	J	168	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
44	2	3605/5025 (71%)	2056 (57%)	325 (9%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
45	3	156/194 (80%)	81 (51%)	6 (3%)
46	4	118/121 (97%)	69 (58%)	9 (7%)
All	All	3879/5340 (72%)	2206 (56%)	340 (8%)

5 of 2206 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
44	2	2	G
44	2	3	C
44	2	5	A
44	2	6	C
44	2	8	U

5 of 340 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
44	2	3873	G
44	2	4659	U
44	2	4033	G
44	2	4338	A
44	2	4740	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

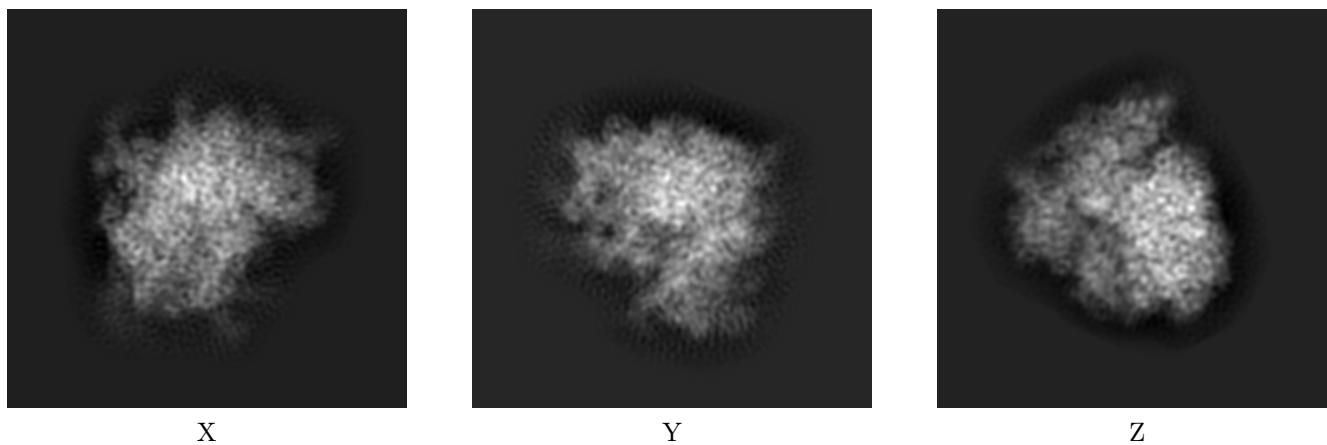
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2813. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

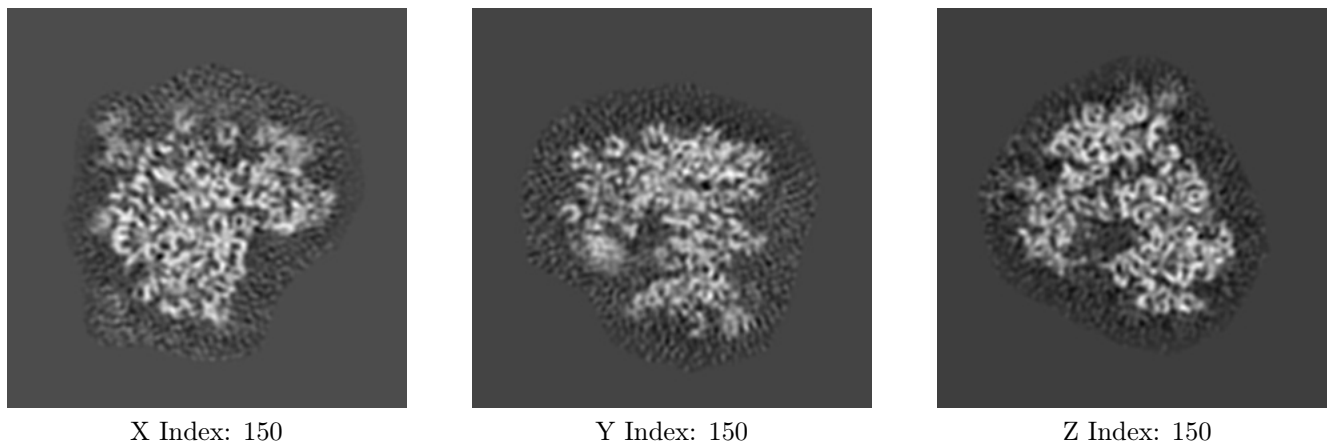
6.1.1 Primary map



The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

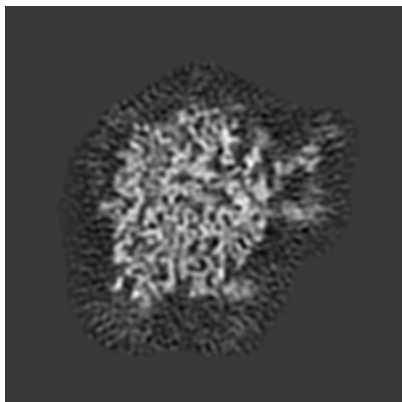
6.2.1 Primary map



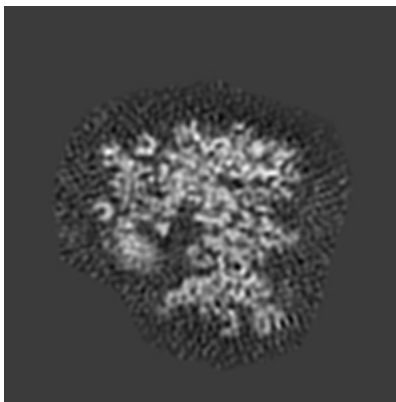
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

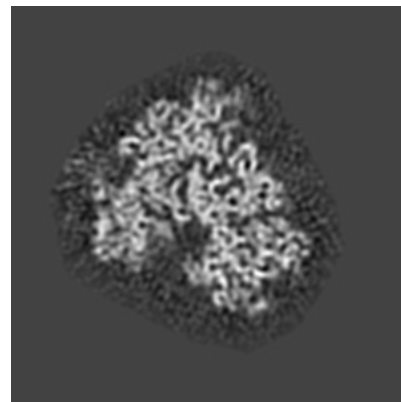
6.3.1 Primary map



X Index: 172



Y Index: 149

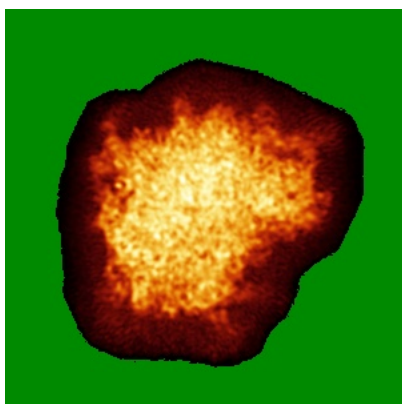


Z Index: 154

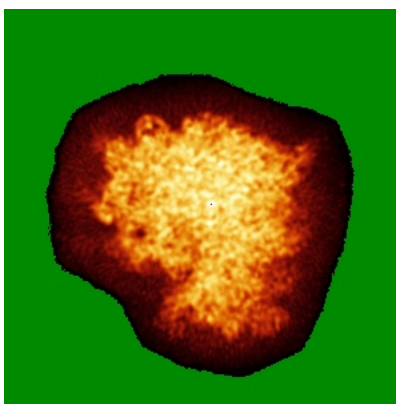
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

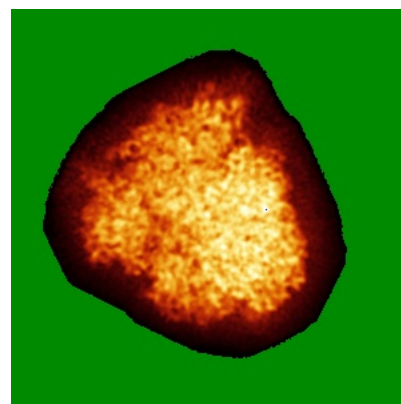
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

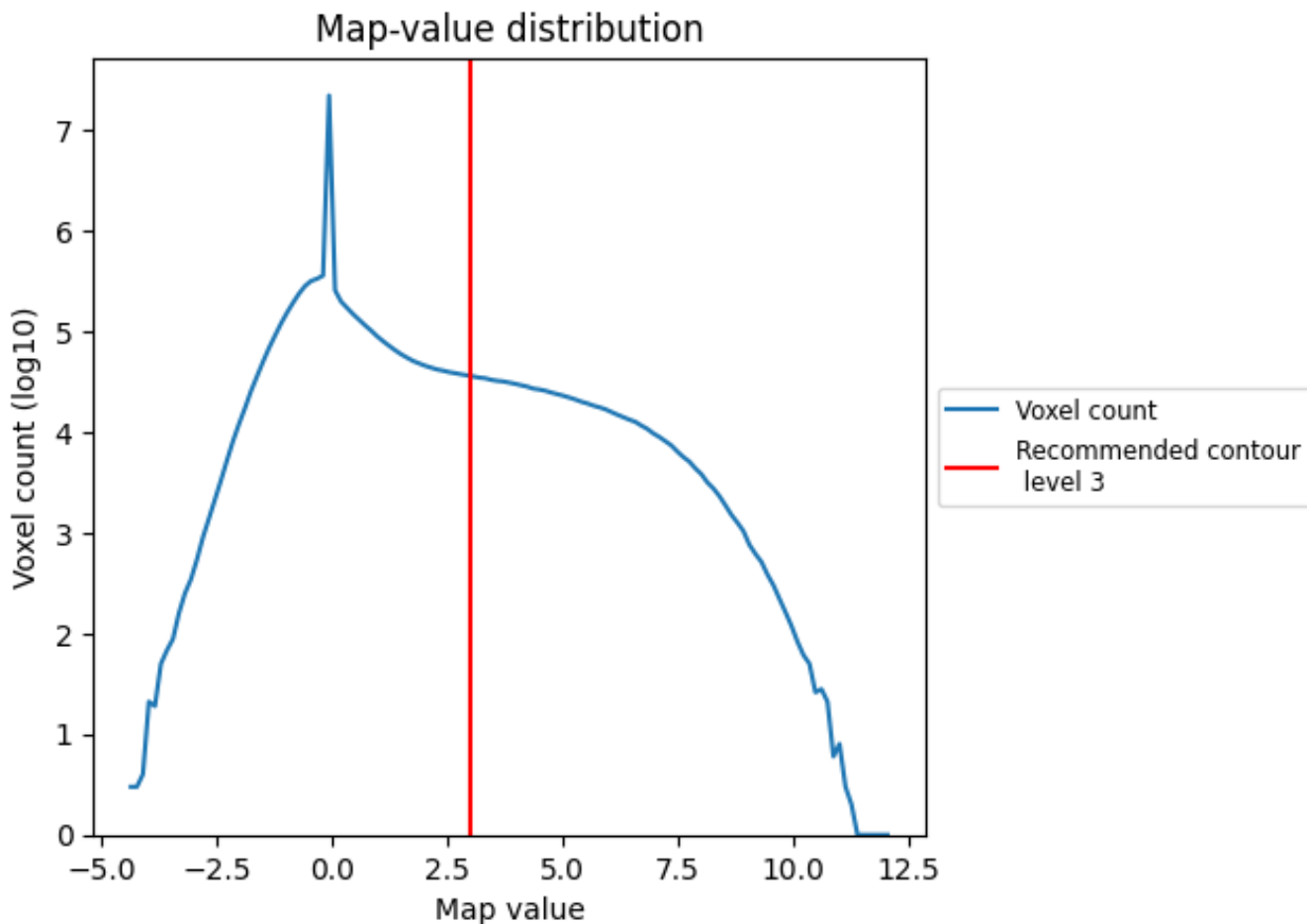
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

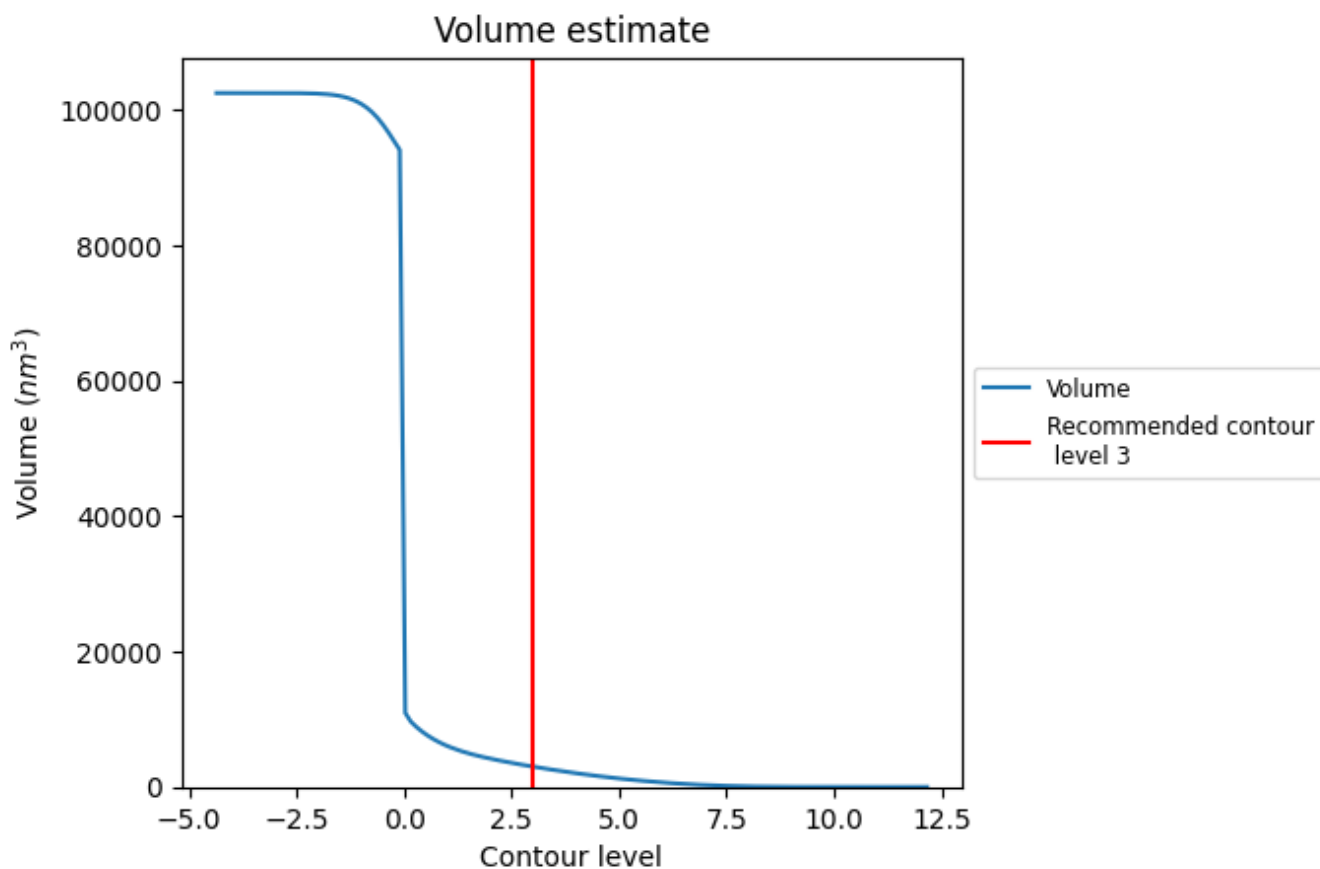
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

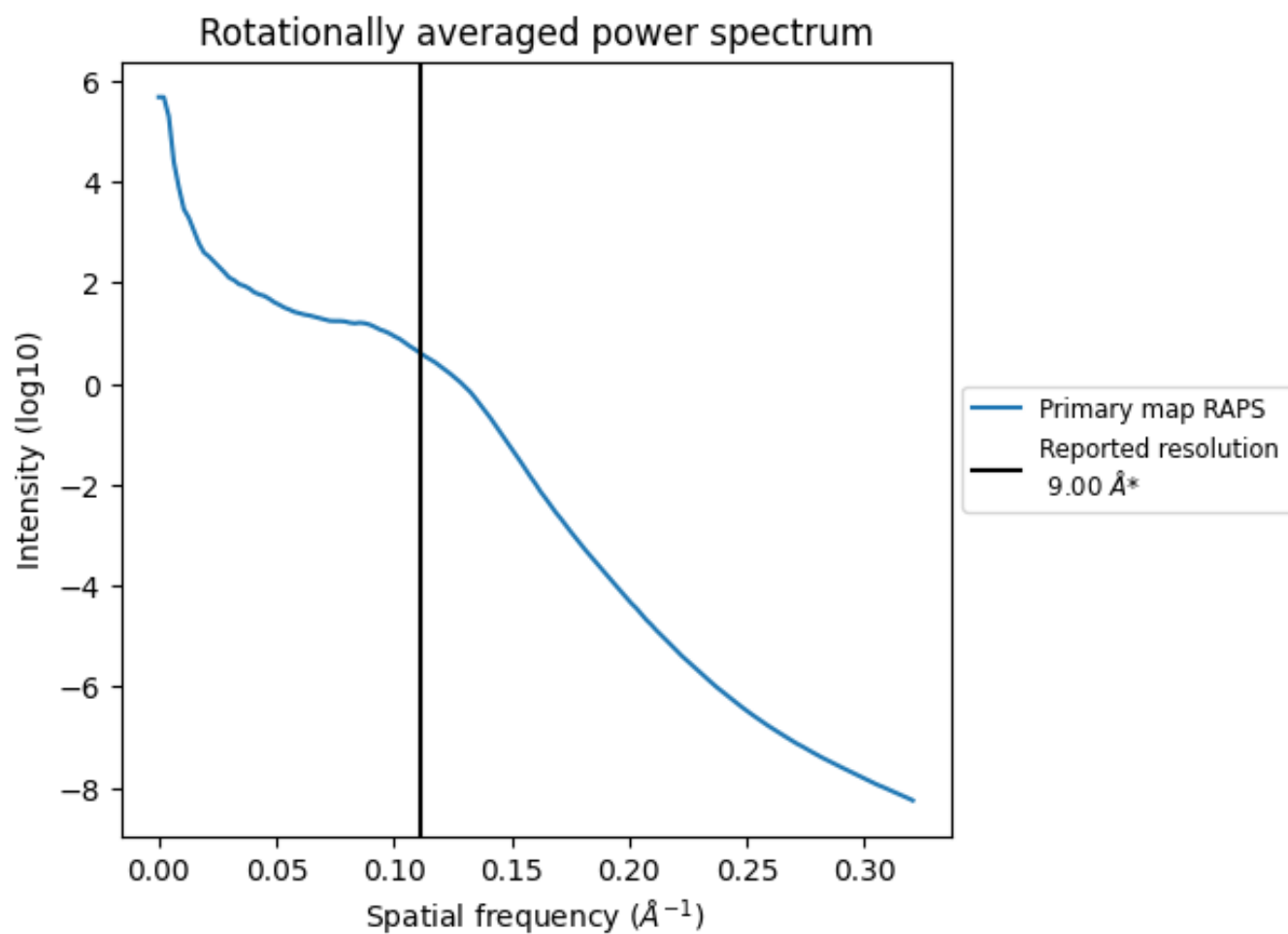
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 3001 nm³; this corresponds to an approximate mass of 2711 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.111 Å⁻¹

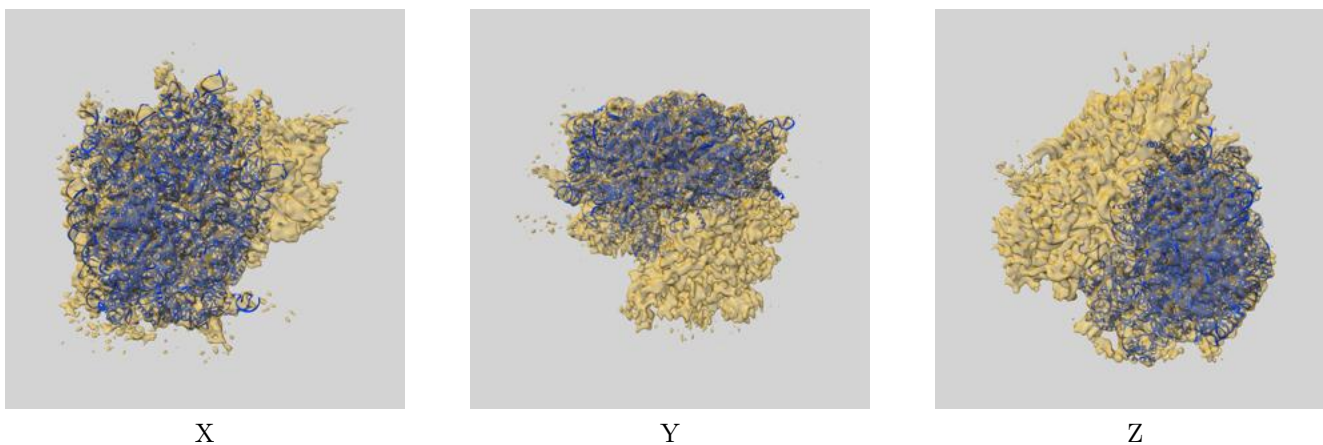
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

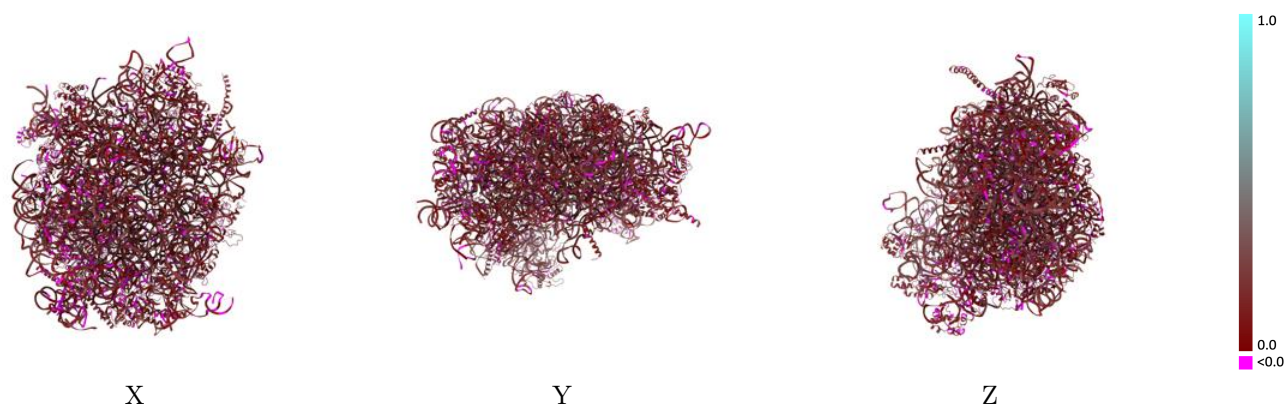
This section contains information regarding the fit between EMDB map EMD-2813 and PDB model 4D67. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



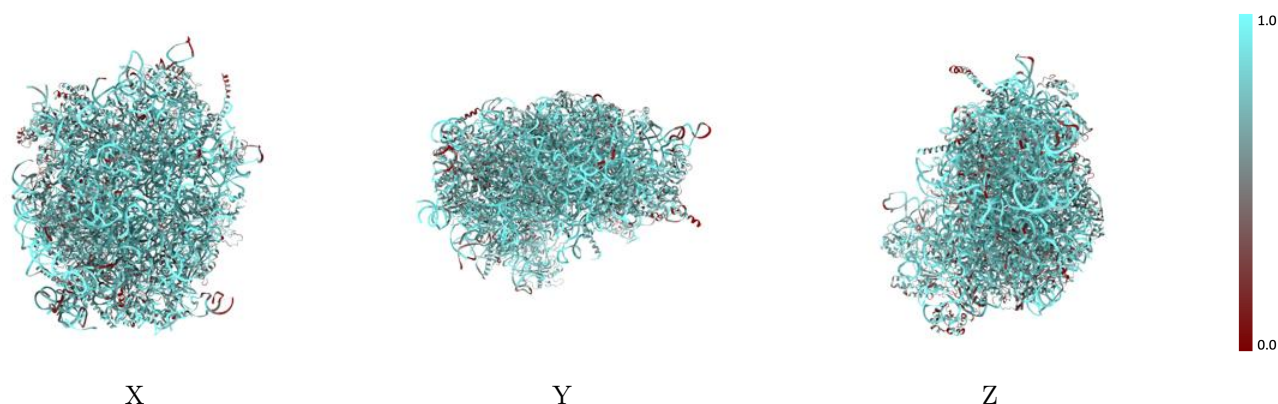
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [\(i\)](#)



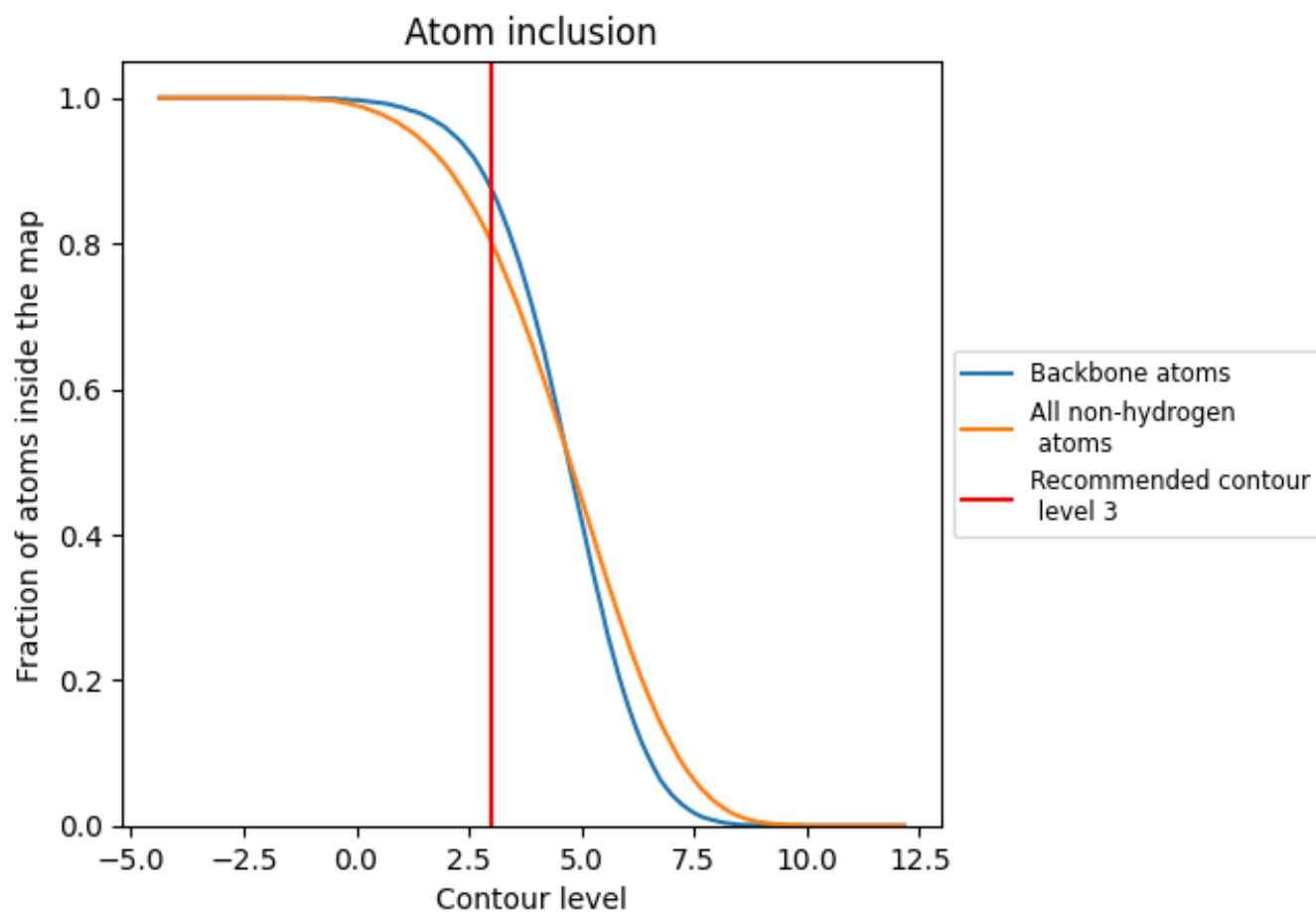
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3).







































































9.4 Atom inclusion [i](#)

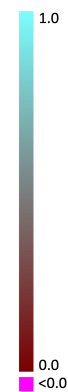


At the recommended contour level, 88% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

























The table lists the average atom inclusion at the recommended contour level (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8020	 0.1420
2	 0.8830	 0.1660
3	 0.9030	 0.1700
4	 0.9460	 0.1820
A	 0.6610	 0.0870
B	 0.6850	 0.0980
C	 0.6880	 0.0900
D	 0.6680	 0.1060
E	 0.6070	 0.0930
F	 0.6510	 0.1020
G	 0.6610	 0.1250
H	 0.7150	 0.1300
I	 0.6590	 0.1180
J	 0.7330	 0.1140
L	 0.6350	 0.1020
M	 0.7010	 0.1110
N	 0.6780	 0.0780
O	 0.6870	 0.1080
P	 0.6970	 0.0890
Q	 0.6580	 0.0980
R	 0.6720	 0.1170
S	 0.6820	 0.1090
T	 0.6660	 0.1050
U	 0.6230	 0.1370
V	 0.6310	 0.1120
W	 0.6860	 0.1100
X	 0.6350	 0.1070
Y	 0.7010	 0.1080
Z	 0.6830	 0.1160
a	 0.6760	 0.1000
b	 0.7040	 0.1090
c	 0.6310	 0.1200
d	 0.7100	 0.1200
e	 0.6480	 0.1020
f	 0.6590	 0.0690



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Chain	Atom inclusion	Q-score
g	 0.6830	 0.0980
h	 0.6620	 0.1140
i	 0.6600	 0.1260
j	 0.7530	 0.0940
k	 0.5880	 0.1300
l	 0.7630	 0.1260
m	 0.6980	 0.1130
n	 0.6470	 0.1010
o	 0.5870	 0.0950
p	 0.6620	 0.1090
t	 0.6670	 0.0860
u	 0.4880	 0.0770